

Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995
 DEFINITION Human DNase I mRNA, complete cds.
 ACCESSION M55983
 VERSION M55983.1 GI:181623
 KEYWORDS DNase I.
 SOURCE Human pancreas, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 FEATURES Location/Qualifiers
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 /gene="DNase I"
CDS 160..1008
 /gene="DNase I"
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 /product="DNase I"
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mat peptide 226..1005
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 121 cattctcgccatctctgagg acatcacatcatctcggat tgaggggcat gaagctgctg
 181 gggcgctgc tggcactggc gcccctactg cagggggccg tgcgtccctgaa gatcgcc
 241 ttcaacatcc agacatttgg ggagaccaag atgtccaaatgc caccctcgat cagctacatt
 301 gtgcagatcc tgaggcgcta tgacatcgcc ctggtcagg agtgcagaga cagccacctg
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 421 gtggtcagtgc acccactggg acggaacaggc tataaggagc gtcacctgtt cgtgtacagg
 481 cctgaccagg tgtctcggtt ggacagctac tactacatg atggctgcga gcccctgcgg
 541 aacgacaccc tcaaccggaga gccaggccatt gtcagggttct tctcccggtt cacagaggc
 601 agggagtttgc ccattgttcc cctgcgtgc gccccgggggg acgcaggtagc cgagatcgac
 661 gctctctatgc acgtctacccatgtgtccaa gagaaatgggg cttggagga cgtcatgttgc
 721 atggggcgact tcaatgcggg ctgcagctatgtgagaccct cccagtggtc atccatccgc
 781 ctgtggacaa gccccacccatgttcc ccaatggatgttgcgttgcgtcc gggccgtt
 841 cccacgcact gtgcctatgttcc caggatgttgcgttgcgtcc gggccgtt
 901 gtcccgact cggcttcc cttaacttc caggctgcct atggctgag tgaccaactg
 961 gccaagcca tcagtgcacca ctatccatgttgcgttgcgtcc
 1021 cacaccaggatgttgcag
 //

Fig. 1

Human DNase I construct

LOCUS MHDNASE.DN 783 bp mRNA PRI 06-MAR-1995
DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove Narl site
ACCESSION M55983
NID g181623
KEYWORDS DNase I.
SOURCE Human pancreas, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
FEATURES Location/Qualifiers
source 1..1039
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hDNase-18-1"
/tissue_type="pancreas"
sig_peptide 160..225
/gene="DNase I"
CDS 160..1008
/gene="DNase I"
/codon_start=1
/product="DNase I"
/db_xref="PID:g181624"
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mat_peptide 226..1005
/gene="DNase I"
/product="DNase I"
BASE COUNT 168 a 236 c 220 g 159 t
ORIGIN

1 CTGAAGATCG CAGCCTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
61 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
121 AGAGACAGCC ACCTGACTGC CGTGGGGAAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
241 CTGTTCTGT ACAGGCCCTGA CCAGGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
301 TGCAGGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
361 CGGTTCACAG AGGTCAAGGG A GTTGCCATT GTTCCCCCTGC ATGCGGCCCG GGGGGACGCA
421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
481 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
541 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
661 CTCCGAGGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTA ACTTCCAGGC TGCCTATGGC
721 CTGAGTGAAC AACTGGCCCA AGCCATCAGT GACCACATAC CAGTGGAGGT GATGCTGAAG
781 TGA

//

Fig. 2(A)

LOCUS PAS155_GB. 858 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 source <10..>75 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas [Split]"
 sig_peptide 10..75 /gene="DNase I"
 CDS 10..>75 /gene="DNase I"
 /codon_start="1"
 /product="DNase I"
 /db_xref="PID:g181624"

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 D... [Split]"
 gene 10..>75 /gene="DNase I [Split]"
 frag 76..858 /note="1 to 783 of mod humanDNaseI"
 frag 76..858 /note="1 to 72 of 104linker"
 frag join(76..>129,<131..147) /note="1 to 72 of 103linker [Split]"
 frag join(76..>126,<127..>129,<131..147) /note="1 to 78 of 102linker [Split]"

 BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER
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 61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTGG GGAGACCAAG
 121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
 181 CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
 241 AATCAGGACG CACCAAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
 301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTCGGT GGACAGCTAC
 361 TACTACGATG ATGGCTGCAGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
 421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTG CCATTGTTCC CCTGCATGCG
 481 GCCCCGGGGG ACCGAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
 541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
 601 GTGAGACCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
 661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
 721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACCTTC
 781 CAGGCTGCCT ATGGCCTGAG TGACCAAATG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
 841 GAGGTGATGC TGAAGTGA

//

Fig. 2(B)

pAS6 – light chain

LOCUS HMFG1LC2.D 721 bp DNA
DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (BASES 1 TO 342)
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT SCANNED IN FROM JOURNAL
FEATURES
SITES

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to R133 silent mutation (T in Verhoeyen paper)

BASE COUNT 197 a 202 c 182 g 140 t
ORIGIN ?

x LEADER SEQ
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCGAC
61 ATCCAGATGA CCCAGAGGCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC
121 ACCTGTAAGT CCAGTCAGAG CCTTTATAT AGTAGCAATC AAAAGATCTA CTTGGCCTGG
181 TACCAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA
241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTA CCGACTTCAC CTTCACCATC
301 AGCAGCCTCC AGCCAGAGGA CATGCCACC TACTACTGCC AGCAATATTA TAGATATCCT
361 CGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA CTGTGGCTGC ACCATCTGTC
421 TTCATCTTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG
481 CTGAATAACT TCTATCCCAG AGAGGCCAA GTACAGTGGAA AGGTGGATAA CGCCCTCCAA
541 TCGGGTAACT CCCAGGAGAG TGTACACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAC ACAAAAGTCTA CGCCTGCGAA
661 GTCACCCATC AGGGCCTGAG CTCGCCCCGTC ACAAAAGAGCT TCAACAGGGG AGAGTGTAG
721 A

//

Fig. 3(A)

LOCUS HHMFG1KLC_ 730 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..730 /note="1 to 721 of hHMFG1light chain"
 frag 10..730 /note="1 to 72 of 104linker"
 frag join(10..>63,<65..81) /note="1 to 72 of 103linker [Split]"
 frag join(10..>60,<61..>63,<65..81) /note="1 to 78 of 102linker [Split]"
 BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACACAGC TACAGGTGTC
 61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
 121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
 181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAGC TGCTGATCTA CTGGGCATCC
 241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTG AGCGGTAGCG GTAGCGGTAC CGACTTCACC
 301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
 361 AGATATCCTC GGACGTTCGG CCAAGGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
 601 TACAGCCTCA GCAGCACCCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCCGTCA CAAAGAGCTT CAACAGGGGA
 721 GAGTGTAGA

//

Fig. 3(B)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCIILFLVATATGVHSDIQMTQSPSSLSASVGDRVITCKSSQL
LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT
DFTFTISSLQPEDIAYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTTLSKADYEHKVYACEVTHQGLSSPVTKSFN
RGEC

Fig. 3(C)

pAS6 – heavy chain

LOCUS HHMFG1HC.D 1404 bp DNA
 DEFINITION HUMANISED HMFG1 heavy chain
 ACCESSION HHMFG1H
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT VH domain SCANNED IN FROM JOURNAL
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 333 a 439 c 379 g 253 t
 ORIGIN ?

LEADER

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTC CAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCCTG GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCTC ACACAACTGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CGCGGGAGG AGCACTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGTAA ATGA
  
```

Antibody DNase Fusions Made Here
(eg pAS34---39.)

→ End of lower hinge region of heavy chain. PAPE Amino Acid Seq. Fab'₂ fusions were made at this point.

Those with HYBRID HINGES are altered further up
i.e.

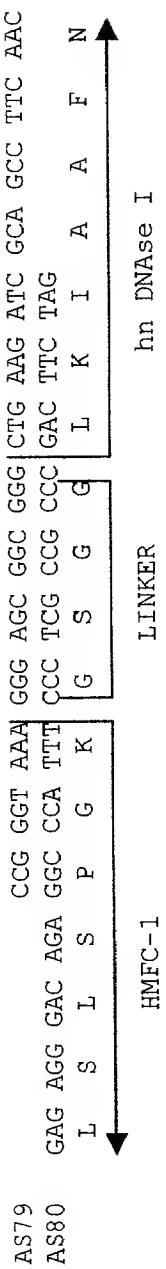
→ This part GACAAAACCTGACACA
D K T H T

After this sequence you get the HYBRID HINGE + LINKER SEQUENCES
Then DNase I (eg Fab-DNase construct pAS302)

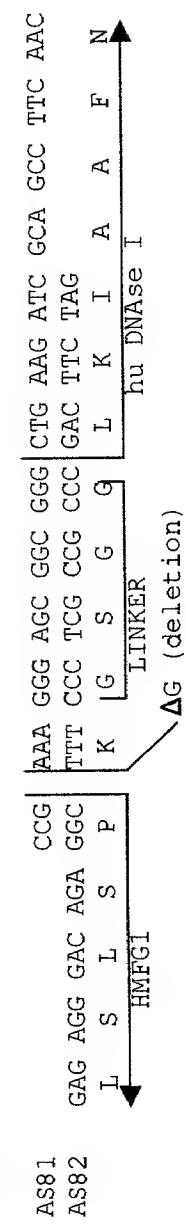
Fig. 3(D)

Oligos involved in the fusion of whole antibody-DNase

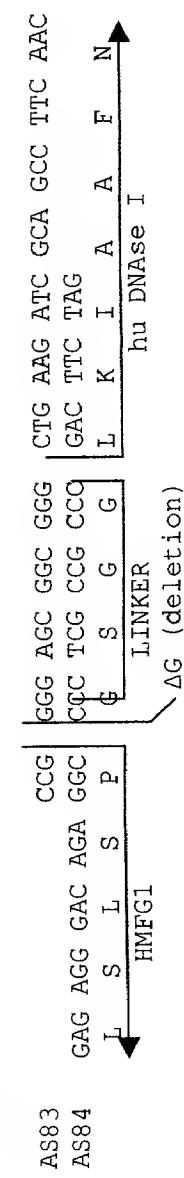
Constructs pAS34/37



Constructs pAS35/38



Constructs pAS36/39



Oligos involved in the fusion of Fab'2-DNaseI

Constructs pAS23/27

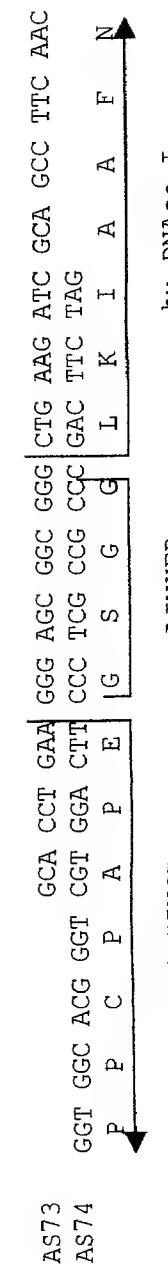
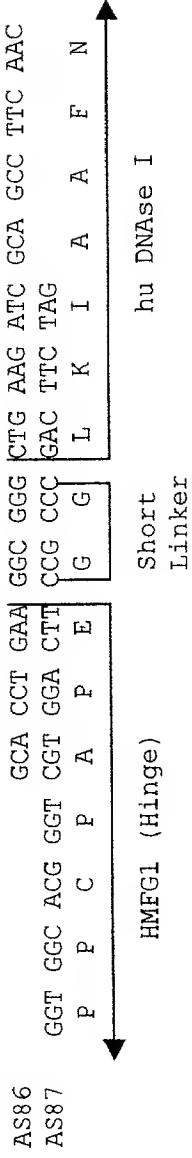


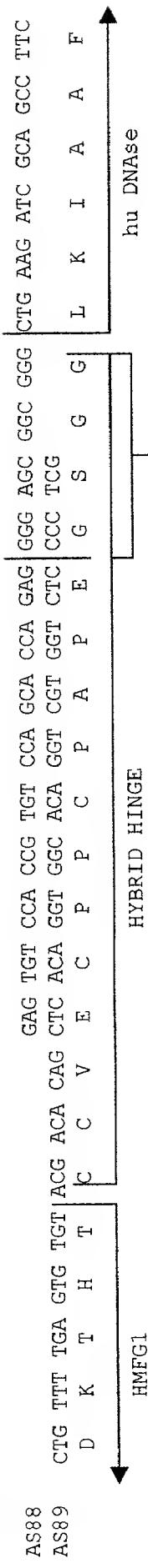
Fig. 4(A)

Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

Constructs pAS101/105



Constructs pAS102/106



Constructs pAS103/107

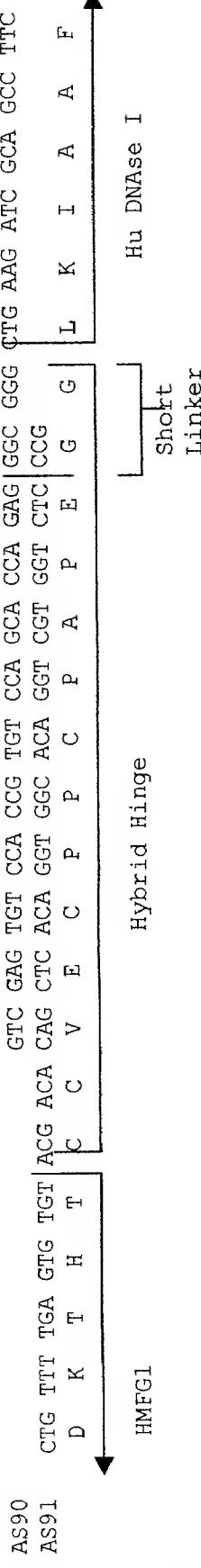


Fig. 4(B)

pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 434 g 308 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAACGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAG **GGAGCGGCAG** GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGGCAC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTGTG
1021 TACAGGCTG ACCAGGTGTC TGCAGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCAGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTCTTCTC CCGGTTCAC
1141 GAGGTCAGGG AGTTGCCAT TGTTCCCTG CATGCGGCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCAGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCTGT GGACAAGCCC CACCTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

//

Fig. 5(A)

LOCUS FDDNASE23_ 1554 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<787..1554)
 /note="1 to 1554 of 23.dna [Split]"
 frag 721..786
 /note="1 to 66 of 23/27linker"
 frag join(721..>735,<736..786)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 344 A 466 C 435 G 309 T 0 OTHER
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 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACATCA
 541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCCG GCTGAAGATC
 781 GCAGCCTTCA ACATCCAGAC ATTTGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
 901 CACCTGACTG CCGTGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTG
 1021 TACAGGCTG ACCAGGTGTC TGCAGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
 1081 TGCGGGAACG ACACCTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCA
 1141 GAGGTCAAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCC CGGGGGACGC AGTAGCCGAG
 1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
 1261 ATGTTGATGG GCGACTTCAA TGCAGGTGGAC AGCTATGTGA GACCCTCCCA GTGGTCATCC
 1321 ATCCGCTGT GGACAAGCCC CACCTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
 1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
 1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
 1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

//

Fig. 5(B)

LOCUS FDDNASE23K 1563 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<796..1563) /note="1 to 1554 of 23.dna [Split]"
 frag 730..795 /note="1 to 66 of 23/27linker"
 frag join(730..>744,<745..795) /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 472 C 437 G 309 T 0 OTHER
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGGA CTCGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCC CTCGAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCAGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACCC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCAGCGGG
 781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 901 AGAGACAGCC ACCTGACTGC CGTGGGGAAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
 961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
 1021 CTGTTCTGTT ACAGGCCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
 1081 TCGGAGCCCT GCGGGAACGA CACCTCAAC CGAGAGCCAG CCATTGTCAAG GTTCTTCTCC
 1141 CGGTTCACAG AGGTCAGGGG GTTGCCATT GTTCCCTGC ATGCGGCCCG GGGGACGCA
 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGGTGTGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
 1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTA ACTTCCAGGC TGCCTATGGC
 1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 1561 TGA

//

Fig. 5(C)

9 18 27 36 45 54

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

Fig. 5(D)
(Sheet 1 of 3)

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	G	S	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E
819	828	837	846	855	864												
ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R
873	882	891	900	909	918												
TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G
927	936	945	954	963	972												
AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V
981	990	999	1008	1017	1026												
AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R
1035	1044	1053	1062	1071	1080												
CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P
1089	1098	1107	1116	1125	1134												
TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C	G	N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R
1143	1152	1161	1170	1179	1188												
TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F	T	E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D
1197	1206	1215	1224	1233	1242												

Fig. 5(D)
(Sheet 2 of 3)

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA

 A V A E I D A L Y D V Y L D V Q E K
 1251 1260 1269 1278 1287 1296
 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT

 W G L E D V M L M G D F N A G C S Y
 1305 1314 1323 1332 1341 1350
 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG

 V R P S Q W S S I R L W T S P T F Q
 1359 1368 1377 1386 1395 1404
 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT

 W L I P D S A D T T A T P T H C A Y
 1413 1422 1431 1440 1449 1458
 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG

 D R I V V A G M L L R G A V V P D S
 1467 1476 1485 1494 1503 1512
 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA

 A L P F N F Q A A Y G L S D Q L A Q
 1521 1530 1539 1548
 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 A I S D H Y P V E V M L K *

Fig. 5(D)
(Sheet 3 of 3)

pAS27

LOCUS PAS27.DNA 1584 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 446 g 310 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
241 GAGAACGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTGCTCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAG **GGAGCGGCCGG** GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTG
1021 TACAGGCCTG ACCAGGTGTC TGCAGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCAGGGAAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTCTACA
1141 GAGGTCAAGGG AGTTGCCAT TGTTCCCTG CATGGGGCCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCAGGTGGAC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTTC CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA **GGGGGGCGGA**
1561 **CCCAAAAGA AGCGCAAGGT TTGA**

//

Fig. 6(A)

LOCUS FDDNASE27_ 1584 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag 721..786
 /note="1 to 66 of 23/27linker"
 frag join(721..>735,<736..786)
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 BASE COUNT 354 A 472 C 447 G 311 T 0 OTHER
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 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
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 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC
 781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
 901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTGTG
 1021 TACAGGCCCTG ACCAGGTGTC TGCAGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
 1081 TGCAGGAAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTACAA
 1141 GAGGTCAAGGG AGTTGCCAT TGTTCCCCCTG CATGCGGCC CGGGGGACGC AGTAGCCGAG
 1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
 1261 ATGTTGATGG GCGACTTCAA TGCAGGTGGAC AGCTATGTGA GACCCTCCCA GTGGTCATCC
 1321 ATCCGGCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
 1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
 1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
 1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GGGGGGCGGA
 1561 CCAAAAAAGA AGCGCAAGGT TTGA

//

Fig. 6(B)

LOCUS FDDNASE27K 1593 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1593
 /note="1 to 1584 of FdDNase27correct"
 frag join(10..>729,<796..1593)
 /note="1 to 1584 of 27.dna [Split]"
 frag 730..795
 /note="1 to 66 of 23/27linker"
 frag join(730..>744,<745..795)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 478 C 449 G 311 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGCTTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCTCTGGTT TGCTTACTGG GGCAAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTCCCC CTGGCACCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTG
 541 TGGAACTCAG GCGCCCTGAC CAGCAGCGT CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCCGG
 781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 901 AGAGACAGCC ACCTGACTGC CGTGGGAAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
 961 GACACCTATC ACTACGTGGT CAGTGAAGCCA CTGGGACGGG ACAGCTATAA GGAGCGCTAC
 1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
 1081 TCGGAGCCT GCAGGGAAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAAG GTTCTCTCC
 1141 CGGTTACAG AGGTCAAGGG GTTGGCATT GTTCCCCTGC ATGCGGCCCG GGGGGACGCA
 1201 TAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
 1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 1441 CTCCGAGGGG CGGTTGTTCC CGACTCGGCT CTTCCCTTA ACTTCCAGGC TGCCTATGGC
 1501 CTGAGTGACC AACTGGCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 1561 GGGGCGGAC CCAAAAGAA GCGCAAGGTT TGA

//

Fig. 6(C)

9	18	27	36	45	54
ATG CGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
M	G	W	S	C	I
I	I	L	F	L	V
A	T	V	A	T	A
T	G	H	V	G	V

63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S	Q	V	Q	L	V
Q	S	G	A	E	V
K	K	P	G	A	S

117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V	K	V	S	C	K
A	S	G	Y	T	F
S	A	Y	W	I	E

171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W	V	R	Q	A	P
G	K	G	L	E	W
E	W	V	G	E	I
L	P				

225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G	S	N	N	S	R
N	E	K	F	K	G
E	R	V	T	V	T
K	G	R	S	V	T
F	I	L	I	L	P

279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GGC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R	D	T	S	T	N
T	A	N	T	A	T
A	Y	M	E	L	S
Y	M	E	L	S	S
M	E	L	S	L	R
E	L	S	S	R	S
L	S	R	S	S	E

333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D	T	A	V	Y	Y
T	A	R	S	Y	D
A	R	S	Y	D	F
V	Y	C	A	F	A
Y	C	A	R	A	W
C	A	R	S	W	F
A	R	S	Y	F	A
R	S	Y	D	A	Y

387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W	G	Q	G	T	L
G	T	V	T	V	S
T	V	S	S	A	S
V	S	S	A	T	K
S	A	S	T	K	G
A	T	K	G	P	P
T	K	G	P	S	S

441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V	F	P	L	A	P
F	P	S	S	K	S
P	S	S	K	S	T
S	K	S	T	S	G
K	S	T	S	G	G
S	T	S	G	G	T
T	S	G	G	T	A
S	G	G	T	A	A
G	G	G	A	A	L

495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G	C	L	V	K	D
C	L	V	K	D	Y
L	V	K	D	Y	F
V	K	D	Y	F	P
K	D	Y	F	P	E
D	Y	F	P	E	P
Y	F	P	E	P	V
F	P	E	P	V	T
P	E	P	V	T	V
E	P	V	T	V	S
P	V	T	V	S	W
V	T	V	S	W	N
T	V	S	W	N	S

549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G	A	L	T	S	G
A	L	T	S	G	V
L	T	S	G	V	H
T	S	G	V	H	T
S	G	V	H	T	F
G	V	H	T	F	P
V	H	T	F	P	A
H	T	F	P	A	V
T	F	P	A	V	L
F	P	A	V	L	Q
P	A	V	L	Q	S
A	V	L	Q	S	S
V	L	Q	S	S	G

Fig. 6(D)
(Sheet 1 of 3)

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
E	G	S	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E
819	828	837	846	855	864												
ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R
873	882	891	900	909	918												
TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G
927	936	945	954	963	972												
AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V
981	990	999	1008	1017	1026												
AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R
1035	1044	1053	1062	1071	1080												
CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P
1089	1098	1107	1116	1125	1134												
TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
C	G	N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R
1143	1152	1161	1170	1179	1188												
TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
F	T	E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D
1197	1206	1215	1224	1233	1242												

Fig. 6(D)
(Sheet 2 of 3)

GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA
 A V A E I D A L Y D V Y L D V Q E K
 1251 1260 1269 1278 1287 1296
 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT
 W G L E D V M L M G D F N A G C S Y
 1305 1314 1323 1332 1341 1350
 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG
 V R P S Q W S S I R L W T S P T F Q
 1359 1368 1377 1386 1395 1404
 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT
 W L I P D S A D T T A T P T H C A Y
 1413 1422 1431 1440 1449 1458
 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG
 D R I V V A G M L L R G A V V P D S
 1467 1476 1485 1494 1503 1512
 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA
 A L P F N F Q A A Y G L S D Q L A Q
 1521 1530 1539 1548 1557 1566
 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA
 A I S D H Y P V E V M L K G G G P K
 1575 1584
 AAG AAG CGC AAG GTT TGA 3'
 K K R K V *

Fig. 6D
(Sheet 3 of 3)

pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34
DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file)
REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS79 and AS80
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
SITES Note
BASE COUNT 501 a 677 c 607 g 411 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCCT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
841 TCGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCAGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 ACCAGGTCA GCCTGACCTG CCTGGTCAA GGTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGCAGCC GGAGAACAAAC TACAAGACCA CGCCCTCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCCTCA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
1681 TCTCGGGTGG ACAGCTACTA CTACGATGAT GGCTCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGGTCA CAGAGGTCAG GGAGTTGCC
1801 ATTGTTCCCC TGCAATGCC CCCGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTCCCT TTAACCTCCA GGCTGCCTAT GGCGTGGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

//

Fig. 7(A)

	9	18	27	36	45	54
5'	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	G TG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					
	603	612	621	630	639	648
	CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
	L Y S L S S V V T V P S S S L G T Q					
	657	666	675	684	693	702

Fig. 7(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT

 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC

 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC

 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT

 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC

 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG

 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA

 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG

 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC

 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG

 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG

 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

 D K S R W Q Q G N V F S C S V M H E

Fig. 7(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A L H N H Y T Q K S L S L S P G K <u>G</u>					
1413	1422	1431	1440	1449	1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<u>S</u> <u>G</u> <u>G</u> L K I A A F N I Q T F G E T K					
1467	1476	1485	1494	1503	1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
M S N A T L V S Y I V Q I L S R Y D					
1521	1530	1539	1548	1557	1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
I A L V Q E V R D S H L T A V G K L					
1575	1584	1593	1602	1611	1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L D N L N Q D A P D T Y H Y V V V S E					
1629	1638	1647	1656	1665	1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P L G R N S Y K E R Y L F V Y R P D					
1683	1692	1701	1710	1719	1728
CAG GTG TCT GCG GTG GAC ACC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
Q V S A V D S Y Y Y D D G C E P C G					
1737	1746	1755	1764	1773	1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
N D T F N R E P A I V R F F S R F T					
1791	1800	1809	1818	1827	1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
E V R E F A I V P L H A A P G D A V					
1845	1854	1863	1872	1881	1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A E I D A L Y D V Y L D V Q E K W G					
1899	1908	1917	1926	1935	1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L E D V M L M G D F N A G C S Y V R					
1953	1962	1971	1980	1989	1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P S Q W S S I R L W T S P T F Q W L					
2007	2016	2025	2034	2043	2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
I P D S A D T T A T P T H C A Y D R					

Fig. 7(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106												
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L
2115	2124	2133	2142	2151	2160												
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I
2169	2178	2187	2196														
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S	D	H	Y	P	V	E	V	M	L	K	*						

Fig. 7(B)
(Sheet 4 of 4)

pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35
DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS81 and AS82
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
SITES Note
BASE COUNT 500 a 677 c 606 g 410 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GAAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCCC TGAGGTCACA
841 TCGCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCAGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCTCAG CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAGG GAGCGGGCGGG CTGAAGATCG CAGCCTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTG AGAGACAGCC ACCTGACTGC CGTGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGT ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTCTCC CGGTTCACAG AGGTCAAGGG GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCG GGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCAG TGGTCATCCA TCCGCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACCA AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

//

Fig. 8(A)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

603 612 621 630 639 648

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

L Y S L S S V V T V P S S S L G T Q

657 666 675 684 693 702

Fig. 8(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT

 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC

 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC

 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT

 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC

 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG

 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA

 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTC

 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC

 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG

 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG

 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

 D K S R W Q Q G N V F S C S V M H E

Fig. 8(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A L P N H Y T Q K S L S L S P K <u>G</u> S					
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<u>G</u> G L K I A A F N I Q T F G E T K M					
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S N A T L V S Y I V Q I L S R Y D I					
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A L V Q E V R D S H L T A V G K L L					
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
D N L N Q D A P D T Y H Y V V S E P					
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L G R N S Y K E R Y L F V Y R P D Q					
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V S A V D S Y Y Y D D G C E P C G N					
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
D T F N R E P A I V R F F S R F T E					
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V R E F A I V P L H A A P G D A V A					
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
E I D A L Y D V Y L D V Q E K W G L					
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
E D V M L M G D F N A G C S Y V R P					
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S Q W S S I R L W T S P T F Q W L I					
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
P D S A D T T A I P T H C A Y D R I					

Fig. 8(B)
(Sheet 3 of 4)

2061 2070 2079 2088 2097 2106
 GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

 V V A G M L L R G A V V P D S A L P

 2115 2124 2133 2142 2151 2160
 TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

 F N F Q A A Y G L S D Q L A Q A I S

 2169 2178 2187
 GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 D H Y P V E V M L K *

Fig. 8(B)
(Sheet 4 of 4)

pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-
1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36
DEFINITION Clone 18.24.1 with residue 1392 T > C
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly
(mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS83 and AS84
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES Residue 1392 T > C silent S to S mutation
SITES Note
BASE COUNT 498 a 678 c 605 g 409 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCC CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGCTTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCCTG GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGATGA GCTGACCAAG
1141 AACCAAGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCT TCTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CcCCG **GGGAG CGGCAGG** CTG AAGATCGCAG CCTTCAACAT CCAGACATT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACAGAC ACCTATCACT ACAGGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCTGTACCA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCAG
1741 GAGCCAGCCA TTGTCAAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCGGG GGACGCACTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTGGAG GACGTCACTGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACCC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGGCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGCCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 9(A)

9 18 27 36 45 . 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC

M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

63 72 81 90 99 . 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

117 126 135 144 153 . 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

171 180 189 198 207 . 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

225 234 243 252 261 . 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

279 288 297 306 315 . 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

333 342 351 360 369 . 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

387 396 405 414 423 . 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

441 450 459 468 477 . 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

495 504 513 522 531 . 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

549 558 567 576 585 . 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

603 612 621 630 639 . 648

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

657 666 675 684 693 . 702

Fig. 9(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT

 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC

 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC

 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT

 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC

 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG

 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA

 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG

 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC

 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG

 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG

 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

 D K S R W Q Q G N V F S C S V M H E

Fig. 9(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT	CTG	CAC	AAC	CAC	TAC
ACG	CAG	AAG	AGC	CTC	TCC
CTG	TCC	CTG	TCC	CCG	GGG
-----	-----	-----	-----	-----	-----
A	L	H	N	R	Y
T	Q	K	S	L	S
S	L	S	L	S	P
-----	-----	-----	-----	-----	-----
<u>G</u>	<u>S</u>	<u>G</u>			
1413	1422	1431	1440	1449	1458
GGG	CTG	AAG	ATC	GCA	GCC
TTC	AAC	ATC	CAG	ACA	TTT
GGG	GAG	ACC	ATG	TGG	GAG
-----	-----	-----	-----	-----	-----
<u>G</u>	<u>L</u>	<u>K</u>	<u>I</u>	<u>A</u>	<u>A</u>
F	N	I	Q	T	F
G	E	T	K	M	S
-----	-----	-----	-----	-----	-----
1467	1476	1485	1494	1503	1512
AAT	GCC	ACC	CTC	GTC	AGC
TAC	ATT	GTG	CAG	ATC	CTG
AGC	CGC	TAC	CGC	TAC	GAC
ATC	GCC	ATC	GAC	ATC	GCC
-----	-----	-----	-----	-----	-----
N	A	T	L	V	S
Y	I	V	Q	I	L
S	R	Y	D	I	A
-----	-----	-----	-----	-----	-----
1521	1530	1539	1548	1557	1566
CTG	GTC	CAG	GAG	GTC	AGA
GAC	AGC	CAC	CTG	ACT	GCC
CTG	GTG	GGG	AAG	CTG	CTG
GAC	GTG	AAG	CTG	GAC	GAC
-----	-----	-----	-----	-----	-----
L	V	Q	E	V	R
D	S	H	L	T	A
V	G	K	L	L	D
-----	-----	-----	-----	-----	-----
1575	1584	1593	1602	1611	1620
AAC	CTC	AAT	CAG	GAC	GCA
CCA	GAC	ACC	TAT	AAG	GAG
GAC	ACC	TAC	CTG	CGC	GTG
AGT	GTC	AGT	GTG	GTC	GAG
CCA	CTG	CTG	GTC	AGT	CCA
-----	-----	-----	-----	-----	-----
N	L	N	Q	D	A
P	D	T	Y	H	Y
V	V	S	E	P	L
-----	-----	-----	-----	-----	-----
1629	1638	1647	1656	1665	1674
GGA	CGG	AAC	AGC	TAT	AAG
GAG	CGC	AGC	TAC	GAG	CGC
CGC	TAC	CTG	TTC	GTG	TAC
TAC	CTG	ACT	GTG	TAC	AGG
AGC	GTG	ACT	TAC	GTG	CCT
GAC	GTC	TAT	GTG	AGT	GAC
-----	-----	-----	-----	-----	-----
G	R	N	S	Y	K
E	R	Y	L	F	V
R	P	Y	Y	R	P
-----	-----	-----	-----	-----	-----
1683	1692	1701	1710	1719	1728
TCT	CGG	GTG	GAC	AGC	TAC
TAC	TAC	GAT	GAT	GGC	TGC
GAT	GAT	GGC	TGC	GAG	CCC
GGC	TGC	GAG	TGC	CCC	TGC
GAC	GTC	CCC	GAC	TGC	GGG
AAC	GTG	TTC	GAG	GAC	AAC
GAC	GTC	ATC	AGC	TAC	GAC
-----	-----	-----	-----	-----	-----
S	A	V	D	S	Y
Y	Y	D	D	G	C
D	D	G	C	E	P
G	C	E	P	C	G
N	N	D	D	C	N
D	E	V	V	C	D
-----	-----	-----	-----	-----	-----
1737	1746	1755	1764	1773	1782
ACC	TTC	AAC	CGA	GAG	CCA
CCA	GCC	ATT	GTC	AGG	TTC
GCC	ATT	GTC	TTC	TTC	TCC
GGG	TTC	ACA	GAG	TTC	ACA
TTC	ACA	GAG	GTC	TCC	GAG
-----	-----	-----	-----	-----	-----
T	F	N	R	E	P
A	I	V	P	A	I
V	R	F	F	S	R
R	F	T	F	T	E
F	E	V	V	C	V
-----	-----	-----	-----	-----	-----
1791	1800	1809	1818	1827	1836
AGG	GAG	TTT	GCC	ATT	GTT
GAG	TTT	GCC	ATT	GTC	CAT
CCC	CTG	CAT	GCG	GCC	CCG
CTG	CAT	GCG	GCC	GGG	GAC
CAT	GCG	GCC	GGG	GAC	GCA
GCC	GCA	GTA	GCA	GTA	GCC
GAG	GCA	GTC	GAG	GCA	GAG
-----	-----	-----	-----	-----	-----
R	E	F	A	I	V
A	I	V	P	L	H
I	A	A	A	A	A
A	A	P	G	D	A
V	A	E	D	A	V
A	E	E	D	A	A
E	E	D	A	V	D
-----	-----	-----	-----	-----	-----
1845	1854	1863	1872	1881	1890
ATC	GAC	GCT	CTC	TAT	GAC
GAC	ATG	TTC	TAT	GAC	GTC
ATG	ATG	GTC	TAC	GAT	GTG
GGC	GGC	GTC	CTG	GAT	TGG
GAC	GTC	TAC	GAT	GTC	GAG
-----	-----	-----	-----	-----	-----
I	D	A	L	Y	D
D	V	M	L	M	G
V	M	L	M	G	D
M	L	M	M	D	F
L	M	M	G	F	N
M	G	D	F	N	A
G	D	F	N	A	G
D	N	A	G	C	C
N	A	G	C	S	S
A	G	C	C	Y	Y
G	C	C	S	V	V
C	S	S	Y	R	R
S	Y	Y	R	P	S
-----	-----	-----	-----	-----	-----
1899	1908	1917	1926	1935	1944
GAC	GTC	ATG	TTG	ATG	GGC
GTC	ATG	TTG	ATG	GAC	GAC
ATG	ATG	ATG	GGC	GAC	GGC
GGC	GGC	GGC	GAC	TAT	TAT
GAC	GGC	GGC	TAT	GTG	ACA
ATG	GGC	GGC	ACA	AGA	CCC
GGC	GGC	ACA	AGC	AGA	TCC
-----	-----	-----	-----	-----	-----
D	V	M	L	M	G
V	M	L	M	G	D
M	L	M	G	D	F
L	M	M	D	F	N
M	G	D	F	N	A
G	D	F	N	A	G
D	N	A	G	C	C
N	A	G	C	S	S
A	G	C	C	Y	Y
G	C	C	S	V	V
C	S	S	Y	R	P
S	Y	Y	R	P	S
-----	-----	-----	-----	-----	-----
1953	1962	1971	1980	1989	1998
CAG	TGG	TCA	TCC	ATC	CGC
TGG	TCA	TCC	ATC	CGC	CTG
TCA	TCC	ATC	CGC	CTG	TGG
ATC	CGC	CTG	TGG	ACA	AGC
CGC	CTG	TGG	ACA	AGC	CCC
CTG	TGG	ACA	AGC	CCC	ACC
TGG	ACA	AGC	CCC	ACC	TTC
ACA	AGC	CCC	ACC	TTC	CAG
AGC	CCC	ACC	TTC	CAG	TGG
ATC	CCC	ACC	TTC	TGG	CTG
CTG	ACC	TTC	TTC	CTG	ATC
-----	-----	-----	-----	-----	-----
Q	W	S	S	I	R
W	S	S	I	R	L
S	I	R	L	W	T
I	R	L	W	T	S
R	L	W	T	S	P
L	W	T	S	P	T
W	T	S	P	T	F
T	S	P	T	F	Q
S	P	T	F	Q	W
P	T	F	Q	W	L
T	F	Q	W	L	I
F	Q	W	L	I	P
-----	-----	-----	-----	-----	-----
2007	2016	2025	2034	2043	2052
GAC	AGC	GCT	GAC	AGC	GTC
AGC	GCT	GAC	ACA	AGC	ATC
GCT	GAC	ACA	ACA	AGC	GTG
GAC	ACA	ACA	CCC	AGC	GGG
ACA	ACA	CCC	ACG	CAC	ATC
ACA	CCC	ACG	CAC	TGT	GTG
CCC	ACG	CAC	TGT	GCC	TAT
ACG	TGT	GCC	TAT	GAC	AGG
CAC	GCC	TAT	GAC	AGG	ATC
TGT	GAC	GAC	AGG	ATC	GTG
GAC	GAC	GAC	ATC	GTG	GTG
ATC	GTG	GTG	GTG	GTG	GTG
GTG	GTG	GTG	GTG	GTG	GTG
-----	-----	-----	-----	-----	-----
D	S	A	D	T	T
S	A	D	T	T	A
A	D	T	T	A	T
D	T	T	A	T	P
T	A	T	P	T	H
A	T	P	H	C	A
T	P	H	C	A	Y
P	H	C	A	Y	D
H	C	A	Y	D	R
C	A	Y	D	R	I
A	Y	D	R	I	V
-----	-----	-----	-----	-----	-----

Fig. 9(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V A G M L L R G A V V P D S A L P F					
2115	2124	2133	2142	2151	2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
N F Q A A Y G L S D Q L A Q A I S D					
2169	2178	2187			
CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
H Y P V E V M L K *					

Fig. 9(B)
(Sheet 4 of 4)

pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-
 1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37
 DEFINITION Clone 16.4.2 (same as hcdnase1.dna template file) plus NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly
 (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS79 and AS80
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 511 a 683 c 619 g 413 t
 ORIGIN ?

```

  1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
  61 GTGCAGCTGG TGCACTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
 241 GAGAAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGA CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCACTC
 781 TTCCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
 841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
 901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
 961 CGTGTGGTCA GCGTCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGAGGCC GGAGAACAAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAAGAGC
1381 CTCTCCCTGT CTCCGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCTG
1501 AGCCGCTACG ACATGCCCT GGTCCAGGAG GTCAAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCGAGAGC CAGCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTCCCT TTAACCTCCA GGCTGCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AGGGGGCG GACCCAAAAA GAAGCGCAAG
2221 GTTGAA
```

//

NLS

Fig. 10(A)

	9	18	27	36	45	54
S'	ATG GGA TGG ACC TGT ATC ATC CTC TTC TTG GTC GCA ACA GCT ACA GGT GTC CAC					
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA						
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG						
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT						
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT						
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG						
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC						
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG						
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG						
	V F P L A P S S K S T S G G T A A L					
	495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACC GTG TCG TGG AAC TCA						
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA						
	G A L T S G V H T F P A V L Q S S G					
	603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG						
	L Y S L S S V V T V P S S S L G T Q					
	657	666	675	684	693	702

Fig. 10(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT

 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC

 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC

 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT

 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC

 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG

 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA

 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG

 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC

 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG

 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TCC CTC TAC AGC AAG CTC ACC GTG

 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

 D K S R W Q O G N V F S C S V M H E

Fig. 10(B)
(Sheet 2 of 4)

1359 1368 1377 1386 1395 1404
 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG
 --- --- --- --- --- ---
A L H N H Y T Q K S L S L S P G K G

 1413 1422 1431 1440 1449 1458
 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG
 --- --- --- --- --- ---
S G G L K I A A F N I Q T F G E T K

 1467 1476 1485 1494 1503 1512
 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC
 --- --- --- --- --- ---
M S N A T L V S Y I V Q I L S R Y D

 1521 1530 1539 1548 1557 1566
 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG
 --- --- --- --- --- ---
I A L V Q E V R D S H L T A V G K L

 1575 1584 1593 1602 1611 1620
 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG
 --- --- --- --- --- ---
L D N L N Q D A P D T Y H Y V V S E

 1629 1638 1647 1656 1665 1674
 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC
 --- --- --- --- --- ---
P L G R N S Y K E R Y L F V Y R P D

 1683 1692 1701 1710 1719 1728
 CAG GTG TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG
 --- --- --- --- --- ---
Q V S A V D S Y Y Y D D G C E P C G

 1737 1746 1755 1764 1773 1782
 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA
 --- --- --- --- --- ---
N D T F N R E P A I V R F F S R F T

 1791 1800 1809 1818 1827 1836
 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA
 --- --- --- --- --- ---
E V R E F A I V P L H A A P G D A V

 1845 1854 1863 1872 1881 1890
 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
 --- --- --- --- --- ---
A E I D A L Y D V Y L D V Q E K W G

 1899 1908 1917 1926 1935 1944
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
 --- --- --- --- --- ---
L E D V M L M G D F N A G C S Y V R

 1953 1962 1971 1980 1989 1998
 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
 --- --- --- --- --- ---
P S Q W S S I R L W T S P T F Q W L

 2007 2016 2025 2034 2043 2052
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
 --- --- --- --- --- ---
I P D S A D T T A T P T H C A Y D R

Fig. 10(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106																		
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT						
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -						
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L						
2115	2124	2133	2142	2151	2160	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -						
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I						
2169	2178	2187	2196	2205	2214	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	CCC	AAA	AAG	AAG
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -						
S	D	H	Y	P	V	E	V	M	L	K	<u>G</u>	<u>G</u>	<u>G</u>	<u>P</u>	<u>K</u>	<u>K</u>	<u>K</u>						
2223																							
CGC	AAG	GTT	TGA	3'																			
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -						
<u>R</u>	<u>K</u>	<u>V</u>	*																				

Fig. 10(B)
(Sheet 4 of 4)

pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38
DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnae.dna)
COMMENT The fusion was made using overlapping oligos AS81 and AS82
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
SITES Note
BASE COUNT 510 a 683 c 618 g 412 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAACGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCCT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCACTC
781 TTCCTCTTCC CCCCCAAACCA CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAAGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG **GAGCGGGCGGG** CTGAAGATCG CAGCCTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTG AGAGACAGCC ACCTGACTGC CGTGGGAAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGT ACAGGCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCAGGCC GCGGGAAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAAG GTTCTCTCC CGGTTCACAG AGGTCAAGGG GTTTGCATT
1801 GTTCCCCTGC ATGGGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTAA ACTTCCAGGC TGCCTATGGC CTGAGTGAAC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG **GGGGGCGGAC CAAAAAAGAA GCGCAAGGTT**
2221 **TGA**

//

NLS

Fig. 11(A)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

603 612 621 630 639 648

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

L Y S L S S V V T V P S S S L G T Q

657 666 675 684 693 702

Fig. 11(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K
 711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT

 V E P K S C D K T H T C P P C P A P
 765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC

 E L L G G P S V F L F P P K P K D T
 819 828 837 846 855 864
 CTG ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC

 L M I S R T P E V T C V V V D V S H
 873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT

 E D P E V K F N W Y V D G V E V H N
 927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC

 A K T K P R E E Q Y N S T Y R V V S
 981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG

 V L T V L H Q D W L N G K E Y K C K
 1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA

 V S N K A L P A P I E K T I S K A K
 1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG

 G Q P R E P Q V Y T L P P S R D E L
 1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC

 T K N Q V S L T C L V K G F Y P S D
 1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG

 I A V E W E S N G Q P E N N Y K T T
 1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG

 P P V L D S D G S F F L Y S K L T V
 1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

 D K S R W Q Q G N V F S C S V M H E

Fig. 11(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC					
-----	-----	-----	-----	-----	-----
A L H N H Y T Q K S L S L S P K G S					
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG					
-----	-----	-----	-----	-----	-----
<u>G</u> G L K I A A F N I Q T F G E T K M					
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC					
-----	-----	-----	-----	-----	-----
S N A T L V S Y I V Q I L S R Y D I					
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG					
-----	-----	-----	-----	-----	-----
A L V Q E V R D S H L T A V G K L L					
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA					
-----	-----	-----	-----	-----	-----
D N L N Q D A P D T Y H Y V V S E P					
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG					
-----	-----	-----	-----	-----	-----
L G R N S Y K E R Y L F V Y R P D Q					
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC					
-----	-----	-----	-----	-----	-----
V S A V D S Y Y D D G C E P C G N					
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG					
-----	-----	-----	-----	-----	-----
D T F N R E P A I V R F F S R F T E					
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC					
-----	-----	-----	-----	-----	-----
V R E F A I V P L H A A P G D A V A					
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG					
-----	-----	-----	-----	-----	-----
E I D A L Y D V Y L D V Q E K W G L					
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC					
-----	-----	-----	-----	-----	-----
E D V M L M G D F N A G C S Y V R P					
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC					
-----	-----	-----	-----	-----	-----
S Q W S S I R L W T S P T F Q W L I					
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC					
-----	-----	-----	-----	-----	-----
P D S A D T T A T P T H C A Y D R I					

Fig. 11(C)
(Sheet 3 of 4)

2061 2070 2079 2088 2097 2106
 GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

 V V A G M L L R G A V V P D S A L P

 2115 2124 2133 2142 2151 2160
 TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

 F N F Q A A Y G L S D Q L A Q A I S

 2169 2178 2187 2196 2205 2214
 GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC

 D H Y P V E V M L K G G G P K K K R

 2223
 AAG GTT TGA 3'

 K V *

Fig. 11(D)
(Sheet 4 of 4)

pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-
1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39
DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly
(mhdnae.dna)
COMMENT The fusion was made using overlapping oligos AS83 and AS84
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES Residue 1392 T > C silent S to S mutation
SITES Note
BASE COUNT 508 a 684 c 617 g 411 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TCGAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTG TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTGT
721 GACAAAACCTC ACACATGCC ACCGTGCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
841 TCGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGC GTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TCGAAGGTCT CCAACAAAGC CCTCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACACCA GGTGTACACC CTGGCCCCAT CCCGGGATGA GCTGACCAAG
1141 ACCAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGCAGCC GGAGAACAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAACAGC
1381 CTCTCCCTGT CcCCGGGGAG GGGCGGG CTG AAGATCGCAG CCTTCACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCTC GTCAAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACAGAC ACTTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCTGTACCA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCAG
1741 GAGCCAGCCA TTGTCAAGGT CTTCTCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTGGAG GACGTCACTGT TGATGGGCAGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GCGGGACCA AAAAGAAGCG CAAGGTTGA

//

Fig. 12(A)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

603 612 621 630 639 648

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

L Y S L S S V V T V P S S S L G T Q

657 666 675 684 693 702

Fig. 12(B)
(Sheet 1 of 4)

ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T
819	828	837	846	855	864												
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H
873	882	891	900	909	918												
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N
927	936	945	954	963	972												
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S
981	990	999	1008	1017	1026												
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K
1035	1044	1053	1062	1071	1080												
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K
1089	1098	1107	1116	1125	1134												
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L
1143	1152	1161	1170	1179	1188												
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D
1197	1206	1215	1224	1233	1242												
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T
1251	1260	1269	1278	1287	1296												
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V
1305	1314	1323	1332	1341	1350												
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	F	C

Fig. 12(B)
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG ACC GGC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A L H N H Y T Q K S L S L S P G <u>S</u> G					
1413	1422	1431	1440	1449	1458
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
<u>G</u> L K I A A F N I Q T F G E T K M S					
1467	1476	1485	1494	1503	1512
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
N A T L V S Y I V Q I L S R Y D I A					
1521	1530	1539	1548	1557	1566
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L V Q E V R D S H L T A V G K L L D					
1575	1584	1593	1602	1611	1620
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
N L N Q D A P D T Y H Y V V V S E P L					
1629	1638	1647	1656	1665	1674
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
G R N S Y K E R Y L F V Y R P D Q V					
1683	1692	1701	1710	1719	1728
TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S A V D S Y Y D D G C E P C G N D					
1737	1746	1755	1764	1773	1782
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T F N R E P A I V R F F S R F T E V					
1791	1800	1809	1818	1827	1836
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
R E F A I V P L H A A A P G D A V A E					
1845	1854	1863	1872	1881	1890
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
I D A L Y D V Y L D V Q E K W G L E					
1899	1908	1917	1926	1935	1944
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
D V M L M G D F N A G C S Y V R P S					
1953	1962	1971	1980	1989	1998
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
Q W S S I R L W T S P T F Q W L I P					
2007	2016	2025	2034	2043	2052
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
D S A D T T A T P T H C A Y D R I V					

Fig. 12(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106																		
GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC	TTT						
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L	P	F						
2115	2124	2133	2142	2151	2160	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT	GAC
-	-	-	-	-	-	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I	S	D
2169	2178	2187	2196	2205	2214	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	CCC	AAA	AAG	AAG	CGC	AAG
-	-	-	-	-	-	H	Y	P	V	E	V	M	L	K	G	<u>G</u>	<u>G</u>	<u>P</u>	<u>K</u>	<u>K</u>	<u>K</u>	<u>R</u>	<u>K</u>
GTT TGA 3'																							

<u>V</u> *																							

Fig. 12(B)
(Sheet 4 of 4)

pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 343 a 467 c 430 g 308 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGGA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCA GCACCTGAAG **GCGGG**CTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCTATGA CAGGATCGTG GTGCAAGGA TGCTGCTCCG AGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTTC CAGGCTGCCT ATGGCCTGAG TGACCAAATG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Fig. 13(A)

LOCUS FDDNASE101 1548 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<781..1548)
 /note="1 to 1548 of PAS101.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 343 A 465 C 431 G 309 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTGTC GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCCAGAGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTGAGG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCAGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAAGTTCT TCTCCCGGTT CACAGAGGTC
 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCTC CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCTT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Fig. 13(B)

LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1557
 /note="1 to 1548 of FdDNase101correct"
 frag join(10..>729,<790..1557)
 /note="1 to 1548 of PAS101.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCTCTGGTT TGCTTACTGG GGCAAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CGAACCCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGGCC
 721 AAATCTTGTG ACAAAAATCA CACATGTCCA CGTGTCCAG CACAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTGGG GAGACCAAGA TGTCCAATGC CACCCCTCGTC
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTT
 1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCAGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTT
 1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCCGGGGGA CGCAGTAGGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
 1261 GTCATGTTGA TGGCCGACTT CAATGCCGGC TGCAGCTATG TGAGACCCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA

//

Fig. 13(C)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

Fig. 13(D)
(Sheet 1 of 3)

603	612	621	630	639	648													
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	S	L	G	T	Q
657	666	675	684	693	702													
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K	
711	720	729	738	747	756													
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P	
765	774	783	792	801	810													
GAA	GCC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
E	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K	
819	828	837	846	855	864													
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D	
873	882	891	900	909	918													
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L	
927	936	945	954	963	972													
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E	
981	990	999	1008	1017	1026													
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D	
1035	1044	1053	1062	1071	1080													
CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G	
1089	1098	1107	1116	1125	1134													
AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T	
1143	1152	1161	1170	1179	1188													
GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTG	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V	
1197	1206	1215	1224	1233	1242													

Fig. 13(D)
(Sheet 2 of 3)

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC

 A E I D A L Y D V Y L D V Q E K W G
 1251 1260 1269 1278 1287 1296
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA

 L E D V M L M G D F N A G C S Y V R
 1305 1314 1323 1332 1341 1350
 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG

 P S Q W S S I R L W T S P T F Q W L
 1359 1368 1377 1386 1395 1404
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG

 I P D S A D T T A T P T H C A Y D R
 1413 1422 1431 1440 1449 1458
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

 I V V A G M L L R G A V V P D S A L
 1467 1476 1485 1494 1503 1512
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

 P F N F Q A A Y G L S D Q L A Q A I
 1521 1530 1539 1548
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 S D H Y P V E V M L K *

Fig. 13(D)
(Sheet 3 of 3)

pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna) (See Figure 2)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 345 a 469 c 440 g 312 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGCTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTATAAATTG TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACATCA
541 GGCGCCCTGA CCAGCGGCCTG GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATTGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGAGC TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCAGTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCGTTGT TCCCGACTCG GCTCTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA

//

Fig. 14(A)

LOCUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTGCTCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA CGTGGGTGAC CGTCCCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATTTGT
 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACGGGAC GGAACAGCTA TAAGGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCAGGTG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
 1141 TCCCGGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCC TGCAATGCC CCCGGGGGAG
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACGC
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTCCCT TTAACCTCCA GGCTGCCTAT
 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
 1561 AAGTGA

//

Fig. 14(B)

pAS302

LOCUS FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
FEATURES Location/Qualifiers
frag 10..1575
/note="1 to 1566 of FdDNase102correct"
BASE COUNT 346 A 474 C 442 G 313 T 0 OTHER
ORIGIN -
1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGAACACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGCTCTGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCAAGGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTCCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTG
541 TGGAACTCAG GCGCCCTGAC CAGCGCGTG CACACCTTCC CGGCTGTCC ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTG CACCGTGTCC AGCACCAGAG
781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGGGGA GACCAAGATG
841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATGCCCTG
901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGA AGCTGCTGGA CAACCTCAAT
961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGGCTGGGA CAGCTACTAC
1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTCA ACCGAGAGCC AGCCATTGTC
1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAAG GAGTTTGCCA TTGTTCCCCCT GCATCGGCC
1201 CGGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
1261 AAATGGGCT TGGAGGACGT CATGTTGATG GGCAGCTCA ATGCGGGCTG CAGCTATGTG
1321 AGACCCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
1441 GCAGGGATGC TGCTCCGAGG GGCGGTTGTG CCCGACTCGG CTCTTCCCTT TAACTCCAG
1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
1561 GTGATGCTGA AGTGA

//

Fig. 14(C)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

Fig. 14(D)
(Sheet 1 of 3)

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P
765	774	783	792	801	810												
TGC	CCA	GCA	CCT	GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C	P	A	P	E	G	S	G	G	L	K	I	A	A	F	N	I	Q
819	828	837	846	855	864												
ACA	TTT	GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	F	G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q
873	882	891	900	909	918												
ATC	CTG	AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
I	L	S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L
927	936	945	954	963	972												
ACT	GCC	GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	A	V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y
981	990	999	1008	1017	1026												
CAC	TAC	GTG	GTC	AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
H	Y	V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L
1035	1044	1053	1062	1071	1080												
TTC	GTG	TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F	V	Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D
1089	1098	1107	1116	1125	1134												
GGC	TGC	GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
G	C	E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R
1143	1152	1161	1170	1179	1188												
TTC	TTC	TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F	F	S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A
1197	1206	1215	1224	1233	1242												

Fig. 14(D)
(Sheet 2 of 3)

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT
 A P G D A V A E I D A L Y D V Y L D
 1251 1260 1269 1278 1287 1296
 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG
 V Q E K W G L E D V M L M G D F N A
 1305 1314 1323 1332 1341 1350
 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC
 G C S Y V R P S Q W S S I R L W T S
 1359 1368 1377 1386 1395 1404
 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG
 P T F Q W L I P D S A D T T A T P T
 1413 1422 1431 1440 1449 1458
 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT
 H C A Y D R I V V A G M L L R G A V
 1467 1476 1485 1494 1503 1512
 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC
 V P D S A L P F N F Q A A Y G L S D
 1521 1530 1539 1548 1557 1566
 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
 Q L A Q A I S D H Y P V E V M L K *

Fig. 14(D)
(Sheet 3 of 3)

pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 436 g 312 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACACTA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATTGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCCCTC
841 GTCAGCTACA TTGTGAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCTAGA
901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCGTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
1141 TTACACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCTGT TGATGGCGA CTTCAATGCG GGCCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCSTAT GACAGGGATCG TGGTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAAC TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 15(A)

LOCUS FDDNASE103 1560 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1560)
 /note="1 to 1560 of PAS103.dna [Split]"
 frag 721..792
 /note="1 to 72 of 103/107linker"
 frag join(721..>771,<772..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 344 A 467 C 436 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCC CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTTC TAGATACAAT
 241 GAGAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTG TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGCAGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTGAGGTT CTTCTCCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAAGT TCCAGGCTGC CTATGGCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 15(B)

LOCUS FDDNASE103 1569 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1569 /note="1 to 1560 of FdDNase103correct"
 frag join(10..>729,<802..1569) /note="1 to 1560 of PAS103.dna [Split]"
 frag 730..801 /note="1 to 72 of 103/107linker"
 frag join(730..>780,<781..801) /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 473 C 438 G 313 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATAACAATG AGAACGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT A CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCAAGGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAAATCA CACATGCTGT GTCGAGTGTG CACCGTGTCC AGCACCAGAG
 781 GGCAGGCTGA AGATCGCAGC CTTCAACATC CAGACATTG GGGAGACCAA GATGTCCAAT
 841 GCCACCCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
 901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAAGCTGC TGGACAACCT CAATCAGGAC
 961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
 1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTT
 1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
 1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
 1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
 1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
 1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
 1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
 1561 CTGAAGTGA

//

Fig. 15(C)

9 18 27 36 45 54
 S ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

 M G W S C I I L F L V A T A T G V H
 63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

 S Q V Q L V Q S G A E V K K P G A S
 117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

 V K V S C K A S G Y T F S A Y W I E
 171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

 W V R Q A P G K G L E W V G E I L P
 225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

 G S N N S R Y N E K F K G R V T V T
 279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

 R D T S T N T A Y M E L S S L R S E
 333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

 D T A V Y Y C A R S Y D F A W F A Y
 387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

 W G Q G T L V T V S S A S T K G P S
 441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

 V F P L A P S S K S T S G G T A A L
 495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

 G C L V K D Y F P E P V T V S W N S
 549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

 G A L T S G V H T F P A V L Q S S G

Fig. 15(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC ACC CCC TCC AGC AGC TTG GGC ACC CAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T Y I C N V N H K P S N T K V D F K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
C P A P E G G L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
G TG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V G K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

Fig. 15(D)
(Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA

 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC

 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC

 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT

 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC

 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG

 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 A Q A I S D H Y P V E V M L K *

Fig. 15(D)
(Sheet 3 of 3)

pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
Position 924 G to A by ggg to gag
Linker GR instead of GG (position 777)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 346 a 468 c 434 g 312 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAGCCTG GGGCCTCAGT GAAGGGTGC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCAA TGCCACCC
841 GTCAGCTACA TTGTGAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGACTGCCGT GGAGAACGCTG CTGGACAAACC TCAATCAGGA CGCACCAAGAC
961 ACCTATCACT ACGTGGTCAG TGAGGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
1201 GCGGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGC TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGAACAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 16(A)

LOCUS FDDNASE104 1560 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1560)
 /note="1 to 1560 of PAS104.dna [Split]"
 frag 721..792
 /note="1 to 72 of 104linker"
 frag join(721..>774,<776..792)
 /note="1 to 72 of 103linker [Split]"
 frag join(721..>771,<772..>774,<776..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGGTGTCC
 121 TCGAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CGGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGCAGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCAA TGCCACCCCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCA
 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTGGAG
 1261 GACGTATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTCCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 16(B)

9 18 27 36 45 54

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCG

S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324

AGA GAC ACA TCC ACA AAC ACA GGC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486

GTC TTC CCC CTG GCA CCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594

GGC GGC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGC

G A L T S G V H T F P A V L O S S G

Fig. 16(C)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC	TAC	TCC	CTC	AGC	GTG
L	Y	S	L	S	V
-----	-----	-----	-----	-----	-----
T	Y	S	V	V	T
-----	-----	-----	-----	-----	-----
657	666	675	684	693	702
ACC	TAC	ATC	TGC	AAC	GTG
T	Y	I	C	N	V
-----	-----	-----	-----	-----	-----
V	E	P	K	S	C
-----	-----	-----	-----	-----	-----
711	720	729	738	747	756
GTT	GAG	CCC	AAA	TCT	TGT
G	A	C	T	C	G
-----	-----	-----	-----	-----	-----
V	E	P	K	S	C
-----	-----	-----	-----	-----	-----
765	774	783	792	801	810
TGC	CCA	GCA	CCT	GAA	GGC
G	C	G	C	A	G
-----	-----	-----	-----	-----	-----
C	P	A	P	E	G
-----	-----	-----	-----	-----	-----
819	828	837	846	855	864
GGG	GAG	ACC	AAG	ATG	TCC
G	G	A	A	T	C
-----	-----	-----	-----	-----	-----
G	E	T	K	M	S
-----	-----	-----	-----	-----	-----
873	882	891	900	909	918
AGC	CGC	TAC	GAC	ATC	GCC
A	C	T	G	A	C
-----	-----	-----	-----	-----	-----
S	R	Y	D	I	A
-----	-----	-----	-----	-----	-----
927	936	945	954	963	972
GTG	GAG	AAG	CTG	CTG	GAC
G	G	A	C	C	A
-----	-----	-----	-----	-----	-----
V	E	K	L	L	D
-----	-----	-----	-----	-----	-----
981	990	999	1008	1017	1026
GTG	GTC	AGT	GAG	CCA	CTG
G	G	A	C	C	G
-----	-----	-----	-----	-----	-----
V	V	S	E	P	L
-----	-----	-----	-----	-----	-----
1035	1044	1053	1062	1071	1080
TAC	AGG	CCT	GAC	CAG	GTG
T	A	C	G	C	T
-----	-----	-----	-----	-----	-----
Y	R	P	D	Q	V
-----	-----	-----	-----	-----	-----
1089	1098	1107	1116	1125	1134
GAG	CCC	TGC	GGG	AAC	GAC
G	C	G	G	A	G
-----	-----	-----	-----	-----	-----
E	P	C	G	N	D
-----	-----	-----	-----	-----	-----
1143	1152	1161	1170	1179	1188
TCC	CGG	TTC	ACA	GAG	GTC
S	R	F	T	E	V
-----	-----	-----	-----	-----	-----
S	R	F	T	E	V
-----	-----	-----	-----	-----	-----

6 1215 1224

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA

 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC

 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC

 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT

 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC

 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG

 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

 A Q A I S D H Y P V E V M L K *

Fig. 16(C)
(Sheet 3 of 3)

pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(pAS105)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASe1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 353 a 473 c 442 g 310 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCC TTGAGTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAAGTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCCT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCCT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTGT
721 GACAAAACTC ACACATGCC ACCGTGCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTGAG GGAGACCAAG ATGTCCAATG CCACCCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGAGC CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGG ACAGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTGA

//

→ NLS

Fig. 17(A)

LOCUS FDDNASE105 1578 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<781..1578)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 721..780
 /note="1 to 60 of 101/105linker"
 frag join(721..>735,<736..>759,<760..>780)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 353 A 471 C 443 G 311 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCCT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCTC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCCAGAGG GCGGGCTGAA GATCGCAGCC
 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCCTGT CAGCTACATT
 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAAGA CAGCCACCTG
 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
 961 GTGGTCAGTG AGCCACTGGG ACGBAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAAGGTTCT TCTCCCGTT CACAGAGGTC
 1141 AGGGAGTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
 1201 GCTCTCTATG ACGTCTACCT GGATGTCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCCT CCCAGTGGTC ATCCATCCGC
 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
 1441 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGG CGGACCCAAA
 1561 AAGAAGCGCA AGGTTGA

//

Fig. 17(B)

LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1587
 /note="1 to 1578 of FdDNase105correct"
 frag join(10..>729,<790..1587)
 /note="1 to 1578 of PAS105.dna [Split]"
 frag 730..789
 /note="1 to 60 of 101/105linker"
 frag join(730..>744,<745..>768,<769..>789)
 /note="1 to 80 of 102linker [Split]"
 BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER
 ORIGIN -
 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGT CCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAACGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCC CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACTCAG GCGCCCTGAC CAGCGCGTG CACACCTTCC CGGTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGGCC
 721 AAATCTTGTG ACAAAAATCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
 781 ATCGCAGCCT TCAACATCCA GACATTGGG GAGACCAAGA TGTCCAATGC CACCCCTCGTC
 841 AGCTACATTG TGCAAGATCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTT
 1021 GTGTACAGGC CTGACCAGGT GTCTCGGGT GACAGCTACT ACTACGATGA TGGCTGCGAG
 1081 CCCTGCGGGG ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTT
 1141 ACAGAGGTCA GGGAGTTTG CATTGTTCCC CTGCATGCGG CCCCGGGGG CAAGTAGGCC
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
 1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
 1381 ACAGCTACAC CCACCGACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
 1441 GGGGCCGTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCACT TATCCAGTGG AGGTGATGCT GAAGGGGGGC
 1561 GGACCCAAAA AGAACGCAA GGTGTTGA

//

Fig. 17(C)

9 18 27 36 45 54
 5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

 M G W S C I I L F L V A T A T G V H

 63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

 S Q V Q L V Q S G A E V K K P G A S

 117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

 V K V S C K A S G Y T F S A Y W I E

 171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

 W V R Q A P G K G L E W V G E I L P

 225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

 G S N N S R Y N E K F K G R V T V T

 279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

 R D T S T N T A Y M E L S S L R S E

 333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

 D T A V Y Y C A R S Y D F A W F A Y

 387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

 W G Q G T L V T V S S A S T K G P S

 441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

 V F P L A P S S K S T S G G T A A L

 495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

 G C L V K D Y F P E P V T V S W N S

 549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

 G A L T S G V H T F P A V L Q S S G

Fig. 17(D)
(Sheet 1 of 3)

603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765	774	783	792	801	810												
GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K
819	828	837	846	855	864												
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D
873	882	891	900	909	918												
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L
927	936	945	954	963	972												
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E
981	990	999	1008	1017	1026												
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D
1035	1044	1053	1062	1071	1080												
CAG	GTG	TCT	GCG	GPG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G
1089	1098	1107	1116	1125	1134												
AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T
1143	1152	1161	1170	1179	1188												
GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V
1197	1206	1215	1224	1233	1242												

Fig. 17(D)
(Sheet 2 of 3)

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC

 A E I D A L Y D V Y L D V Q E K W G
 1251 1260 1269 1278 1287 1296
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA

 L E D V M L M G D F N A G C S Y V R
 1305 1314 1323 1332 1341 1350
 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG

 P S Q W S S I R L W T S P T F Q W L
 1359 1368 1377 1386 1395 1404
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG

 I P D S A D T T A T P T H C A Y D R
 1413 1422 1431 1440 1449 1458
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

 I V V A G M L L R G A V V P D S A L
 1467 1476 1485 1494 1503 1512
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

 P F N F Q A A Y G L S D Q L A Q A I
 1521 1530 1539 1548 1557 1566
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG

 S D H Y P V E V M L K G G G P K K K
 1575
 CGC AAG GTT TGA 3'

 R K V *

Fig. 17(D)
(Sheet 3 of 3)

pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS (pAS106)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 355 a 475 c 452 g 314 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTAUTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCCT CGGTCTTCCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG TGGAACCTCA
541 GGCGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCACTGAG CCAACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTCGGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCCTGTTCA CAGAGGTCAAG GGAGTTGCC ATTGTTCCCC TGCACTGGGCCC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGAGC TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTCC
1321 CAGTGGTCA CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTGTA

//

→ NLS

Fig. 18(A)

LOCUS FDDNASE106 1596 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<799..1596)
 /note="1 to 1596 of PAS106.dna [Split]"
 frag 721..798
 /note="1 to 78 of 102/106linker"
 BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAACGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTG CAGCACCAGA GGGGAGCGGC
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
 961 CCAGACACCT ATCACTACGT GGTCAGTGTG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
 1081 GGCTGCGAGC CCTCGGGAA CGACACCTTC AACCAGAGAC CAGCCATTGT CAGGTTCTTC
 1141 TCCCGGTTCA CAGAGGTCA GGAGTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTC AGTGGCTGAT CCCCAGACAGC
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTCCCT TTAACTTCCA GGCTGCCTAT
 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
 1561 AAGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

//

Fig. 18(B)

LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag 10..1605 /note="1 to 1596 of FdDNase106correct"
 frag join(10..>729,<808..1605) /note="1 to 1596 of PAS106.dna [Split]"
 frag 730..807 /note="1 to 78 of 102/106linker"
 BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER
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 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCCTTC TGGCTACACC TTCAGTGCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGT GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAACGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTAA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGGA CTCTGGTCAC AGTCTCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCT CCTCCAAGAG CACCTCTGGG
 481 GGACACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCCAG AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAAGAG
 781 GGGAGCGGGG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGGGGA GACCAAGATG
 841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATGCCCTG
 901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGAGCTGCTGGA CAACCTCAAT
 961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
 1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
 1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
 1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAAGG GAGTTGCA TTGTCTCCCT GCATGCGGCC
 1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
 1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCAGCTTCA ATGCGGGCTG CAGCTATGTG
 1321 AGACCCTCCC AGTGGTCATC CATCCGCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
 1381 CCCGACAGCG CTGACACCCAG AGCTACACCC ACAGCACTGTG CCTATGACAG GATCGTGGTT
 1441 GCAGGGATGC TGCTCCGAGG GGCGTGTGTT CCCGACTCGG CTCTCCCTT TAACTTCCAG
 1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
 1561 GTGATGCTGA AGGGGGCGG ACCCAAAAAG AAGCGCAAGG TTTGA

//

Fig. 18(C)

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCA GCT ACA GGT GTC CAC					
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					

Fig. 18(D)

(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC ACC CAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
C P A P E G S G G L K I A A F N I Q					
819	828	837	846	855	864
ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T F G E T K M S N A T L V S Y I V Q					
873	882	891	900	909	918
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
I L S R Y D I A L V Q E V R D S H L					
927	936	945	954	963	972
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T A V G K L L D N L N Q D A P D T Y					
981	990	999	1008	1017	1026
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
H Y V V S E P L G R N S Y K E R Y L					
1035	1044	1053	1062	1071	1080
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
F V Y R P D Q V S A V D S Y Y Y D D					
1089	1098	1107	1116	1125	1134
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
G C E P C G N D T F N R E P A I V R					
1143	1152	1161	1170	1179	1188
TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT CGG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
F F S R F T E V R E F A I V P L H Z					
1197	1206	1215	1224	1233	1242

Fig. 18(D)

(Sheet 2 of 3)

GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT

 A P G D A V A E I D A L Y D V Y L D
 1251 1260 1269 1278 1287 1296
 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG

 V Q E K W G L E D V M L M G D F N A
 1305 1314 1323 1332 1341 1350
 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC

 G C S Y V R P S Q W S S I R L W T S
 1359 1368 1377 1386 1395 1404
 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG

 P T F Q W L I P D S A D T T A T P T
 1413 1422 1431 1440 1449 1458
 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT

 H C A Y D R I V V A G M L L R G A V
 1467 1476 1485 1494 1503 1512
 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC

 V P D S A L P F N F Q A A Y G L S D
 1521 1530 1539 1548 1557 1566
 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG

 Q L A Q A I S D H Y P V E V M L K G
 1575 1584 1593
 GGC GGA CCC AAA AAG AAG CGC AAG GTT TGA 3'

 G G P K K K R K V *

Fig. 18(D)

(Sheet 3 of 3)

pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(pAS107)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 448 g 314 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATAAACAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCCT CGGTCTTCCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG **TGTGGAGTGC** **CCACCGTGC** **CAGCACCTGA** **AGGC**GGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAAGA
901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
1561 **GGCGGACCA** **AAAAGAAGCG** **CAAGGTTGA**

//

→ NLS

Fig. 19(A)

LOCUS FDDNASE107 1590 BP SS-DNA SYN 25-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1590)
 /note="1 to 1590 of PAS107.dna [Split]"
 frag 721..792
 /note="1 to 72 of 103/107linker"
 frag join(721..>771,<772..792)
 /note="1 to 78 of 1021linker [Split]"
 BASE COUNT 354 A 473 C 448 G 315 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTAUTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
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 601 TCCCTCAGCA GCGTGGTGAC CGTGCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGT CAGCACCAGA GGGCGGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTG GGGGAGACCA AGATGTCCAA TGCCACCTC
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTAGA
 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGCTTAC CTGGATGTCC AAGAGAAATG GGGCTGGAG
 1261 GACGTCATGT TGATGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCCG TTGTCCCCGA CTCGGCTCTT CCCTTTAAC TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
 1561 GGCAGGACCCA AAAAGAAGCG CAAGGTTGA

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Fig. 19(B)

LOCUS FDDNASE107 1599 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
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 frag join(10..>729,<802..1599)
 /note="1 to 1590 of PAS107.dna [Split]"
 frag 730..801
 /note="1 to 72 of 103/107linker"
 frag join(730..>780,<781..801)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER
 ORIGIN -
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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATT A CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GCCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CGAACCCGGT GACGGTGTG
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTG CACCGTGTCC AGCACCAGAG
 781 GCGGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTG GGGAGACCAA GATGTCCAAT
 841 GCCACCCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
 901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAAGCTGC TGGACAACCT CAATCAGGAC
 961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
 1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
 1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTT CCCTGCATGC GGCCCCGGGG
 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
 1261 GGCTTGGAGG ACGTCATGTT GATGGGGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
 1321 TCCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
 1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
 1441 ATGCTGCTCC GAGGGGCCGT TGTTCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
 1501 TATGGCCTGA GTGACCAACT GGCCCCAGCC ATCAGTGACCC ACTATCCAGT GGAGGTGATG
 1561 CTGAAGGGGG CGGGACCCAA AAAGAACGCGC AAGGTTTGA

//

Fig. 19(C)

	9	18	27	36	45	54
5'	ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GGC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	V F P L A P S S K S T S G G T A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G A L T S G V H T F P A V L Q S S G					

Fig. 19(D)
(Sheet 1 of 3)

	603	612	621	630	639	648												
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG	
- - - - -	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
	657	666	675	684	693	702												
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA	
- - - - -	T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
	711	720	729	738	747	756												
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG	
- - - - -	V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P
	765	774	783	792	801	810												
TGC	CCA	GCA	CCT	GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	
- - - - -	C	P	A	P	E	G	G	L	K	I	A	A	F	N	I	Q	T	F
	819	828	837	846	855	864												
GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	
- - - - -	G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L
	873	882	891	900	909	918												
AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	
- - - - -	S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A
	927	936	945	954	963	972												
GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	
- - - - -	V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y
	981	990	999	1008	1017	1026												
GTG	GTC	AGT	GAG	CCA	CTG	GGG	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	
- - - - -	V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V
	1035	1044	1053	1062	1071	1080												
TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	
- - - - -	Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C
	1089	1098	1107	1116	1125	1134												
GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	
- - - - -	E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R	F	F
	1143	1152	1161	1170	1179	1188												
TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	
- - - - -	S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A	A	P
	1197	1206	1215	1224	1233	1242												

Fig. 19(D)
(Sheet 2 of 3)

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA
 G D A V A E I D A L Y D V Y L D V Q
 1251 1260 1269 1278 1287 1296
 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
 E K W G L E D V M L M G D F N A G C
 1305 1314 1323 1332 1341 1350
 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
 S Y V R P S Q W S S I R L W T S P T
 1359 1368 1377 1386 1395 1404
 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
 F Q W L I P D S A D T T A T P T H C
 1413 1422 1431 1440 1449 1458
 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
 A Y D R I V V A G M L L R G A V V P
 1467 1476 1485 1494 1503 1512
 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
 D S A L P F N F Q A A Y G L S D Q L
 1521 1530 1539 1548 1557 1566
 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA
 A Q A I S D H Y P V E V M L K G G G
 1575 1584
 CCC AAA AAG AAG CGC AAG GTT TGA 3'
 P K K K R K V *

Fig. 19(D)
(Sheet 3 of 3)

Mammalian expression of humanised HMFG1-D Nase constructs

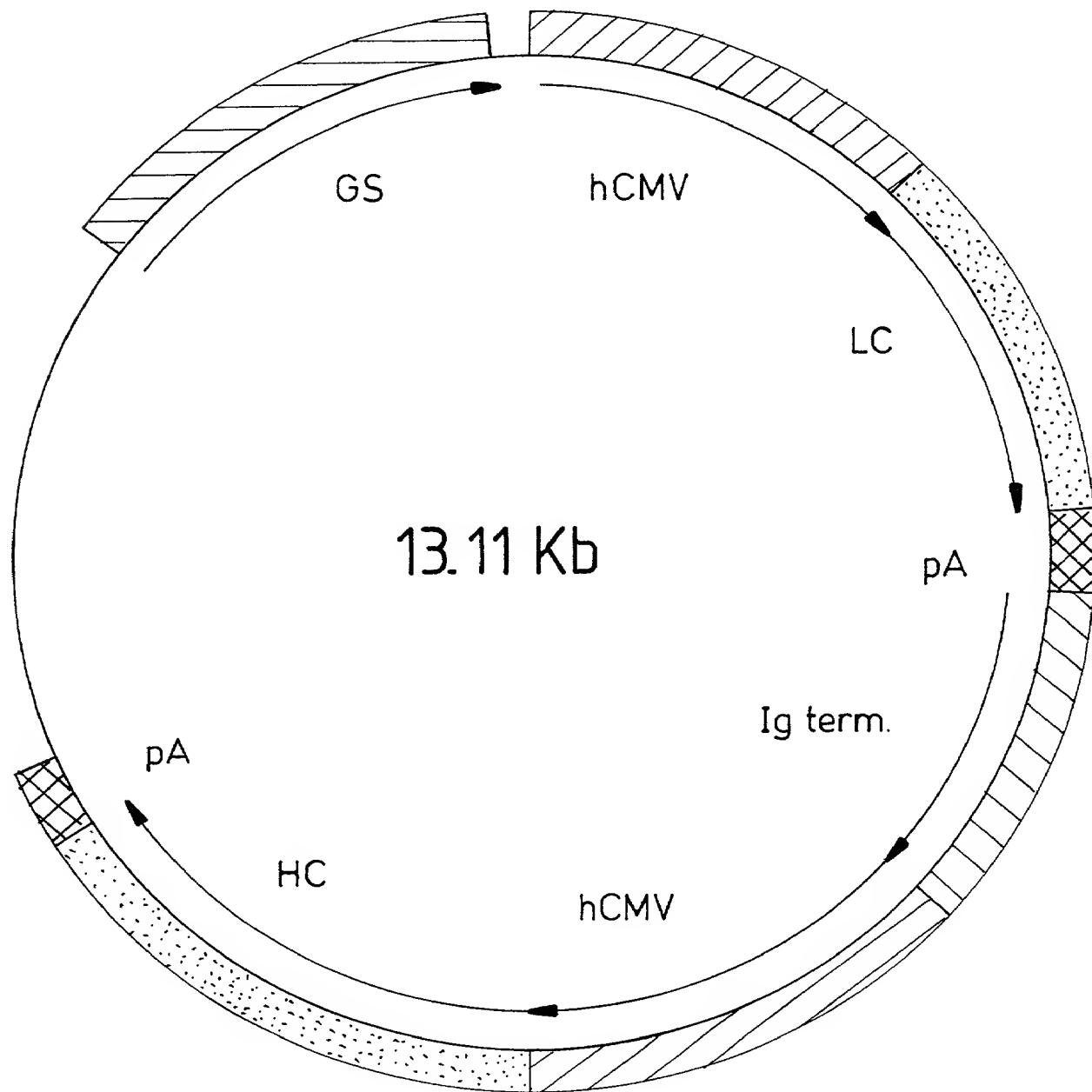
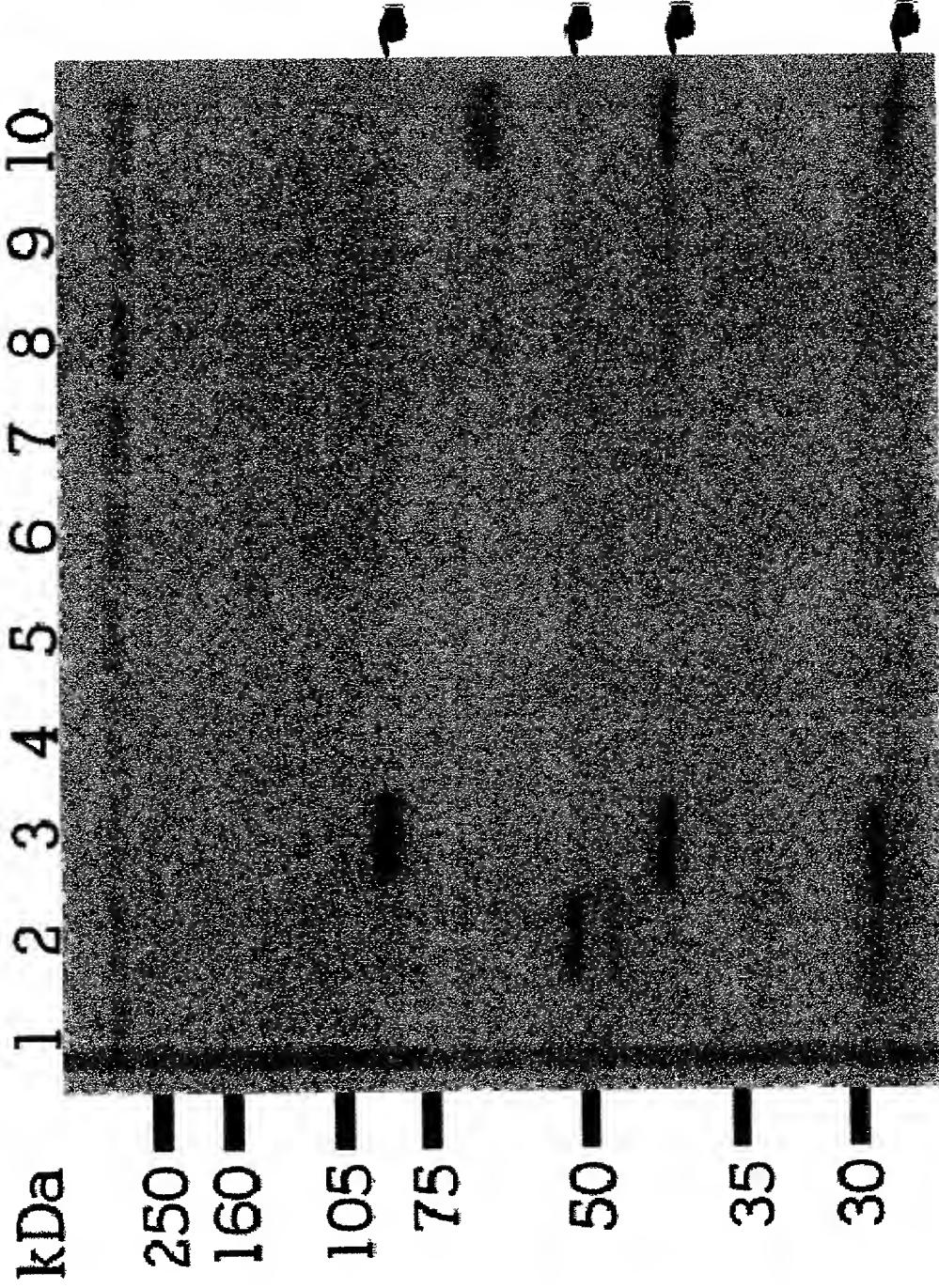


Fig. 20

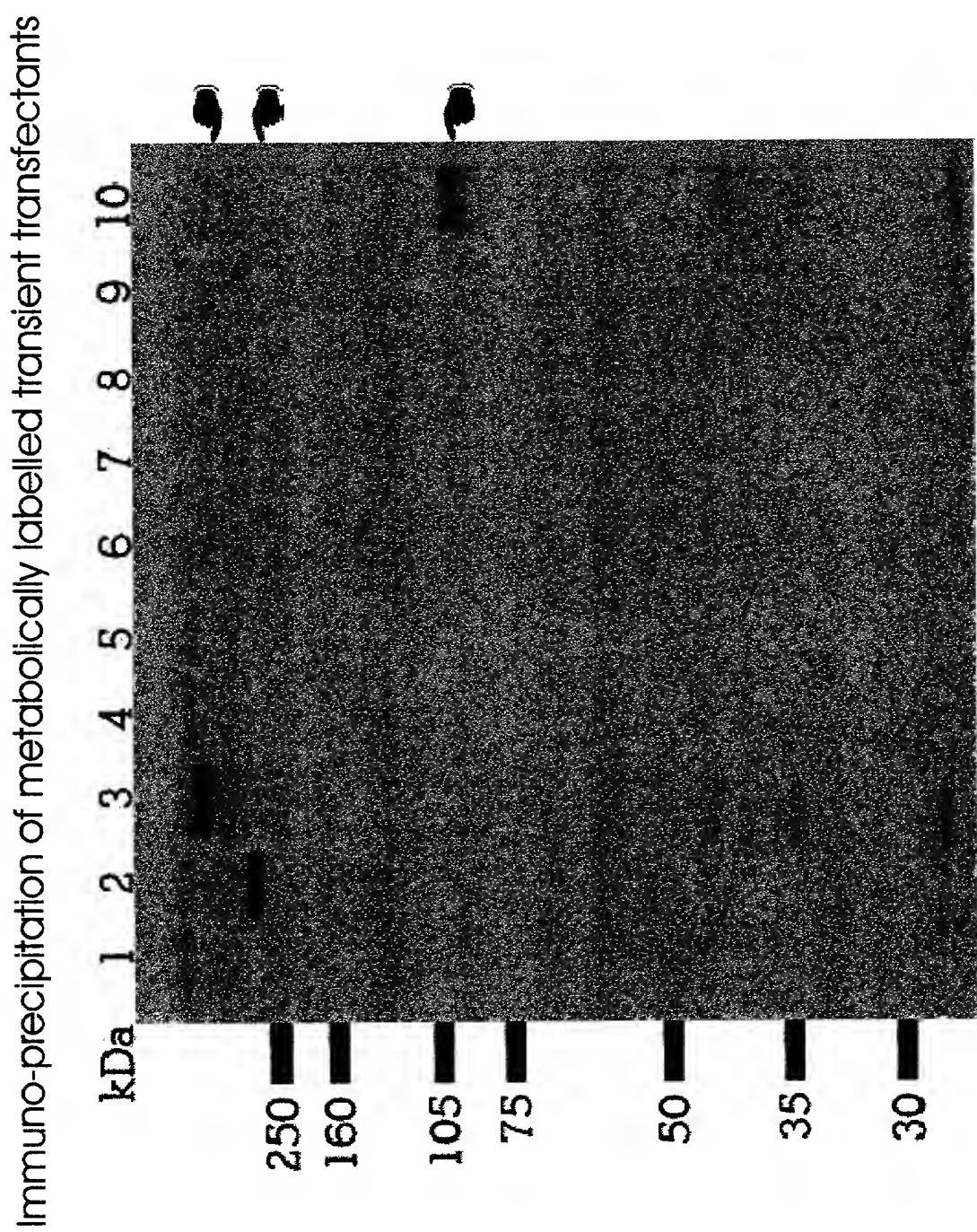
Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE reducing gel

Fig. 21(A)

Fig. 21(B)
8% SDS-PAGE non-reducing gel



Immuno-precipitation of metabolically labelled transient transfectants

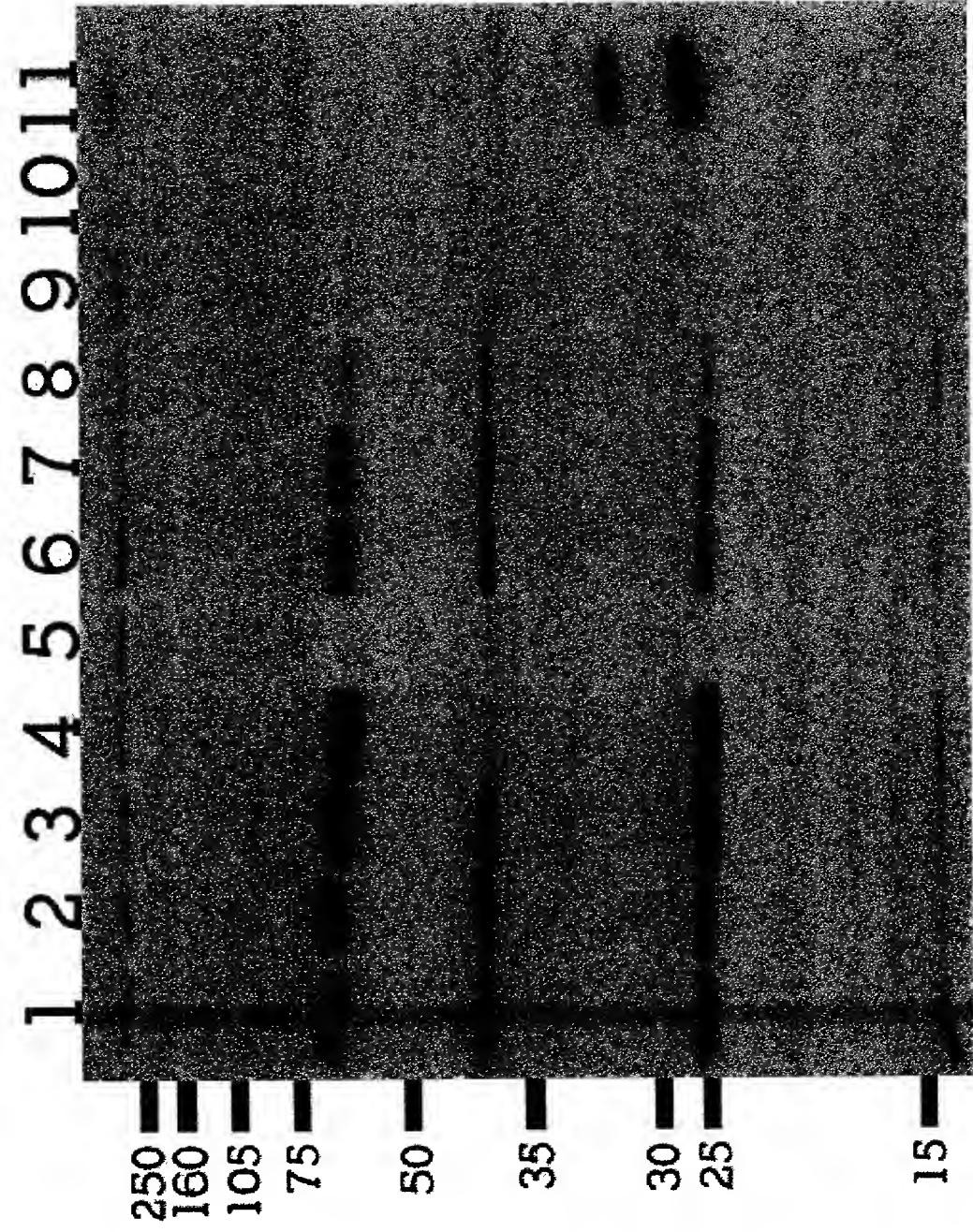


Fig. 21(C) 10% SDS-PAGE reducing gel

Fig. 21(D)

8% SDS-PAGE non-reducing gel

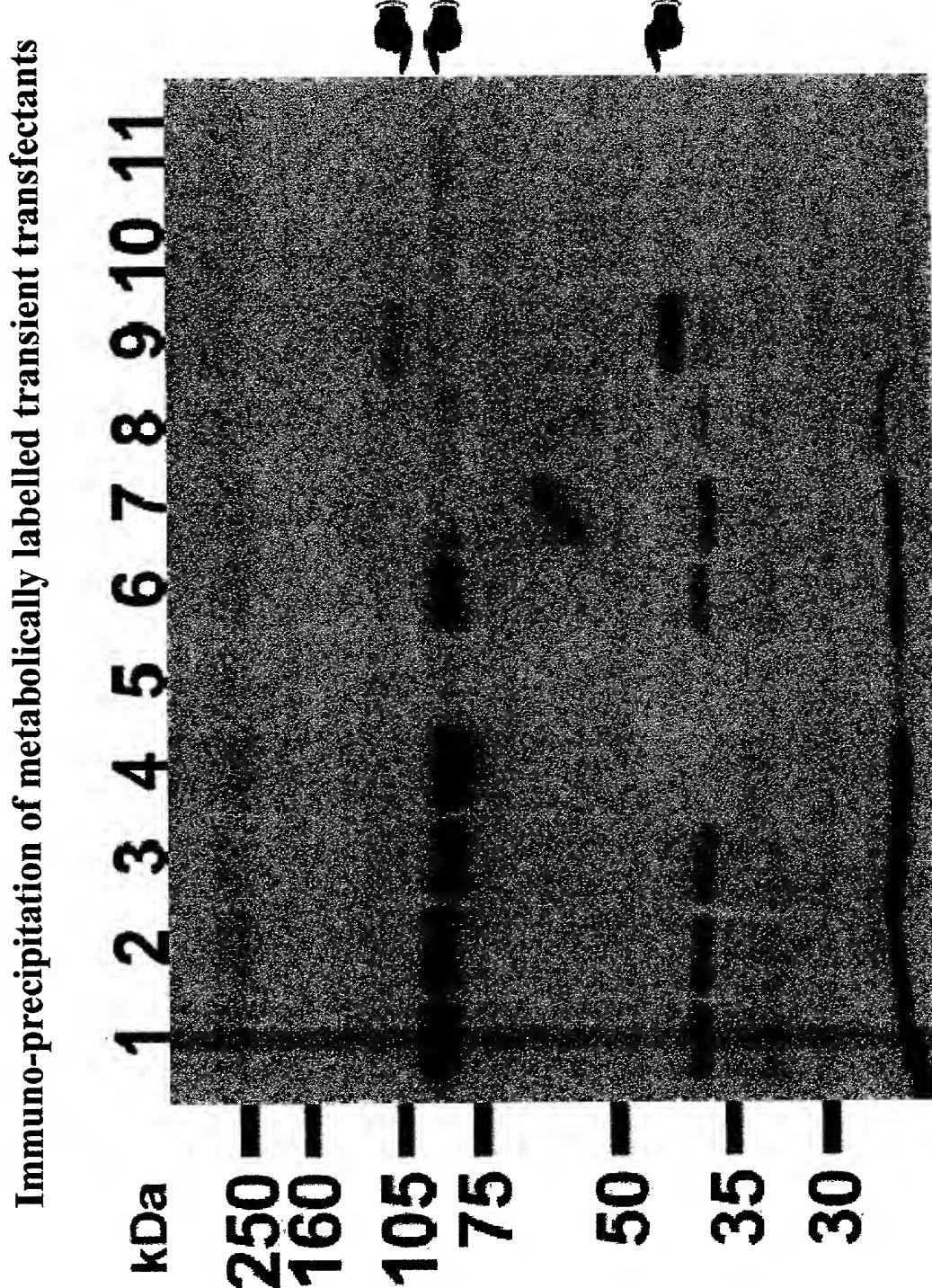


Fig. 22

PDTTRP binding assay standard curve
(5' development)

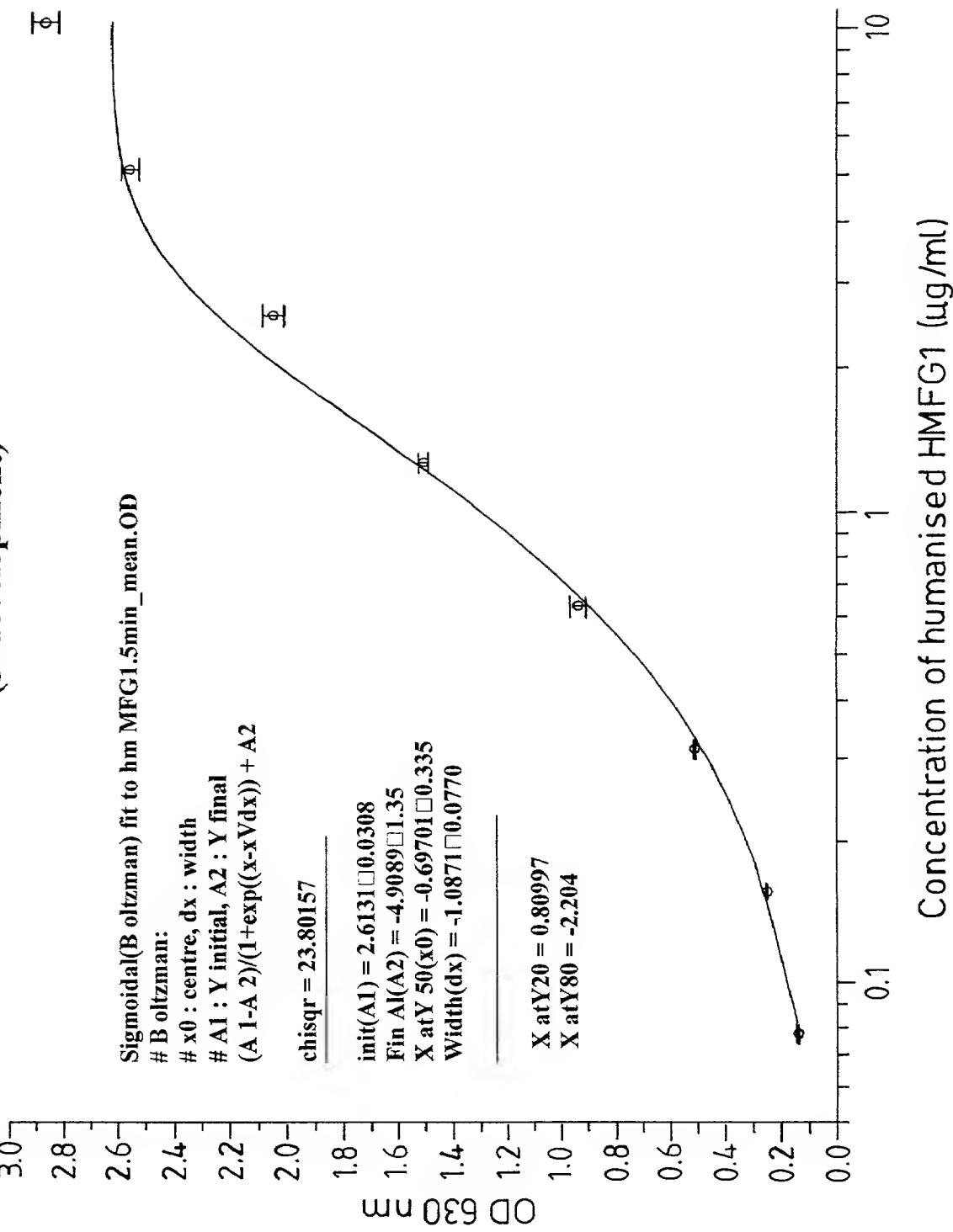
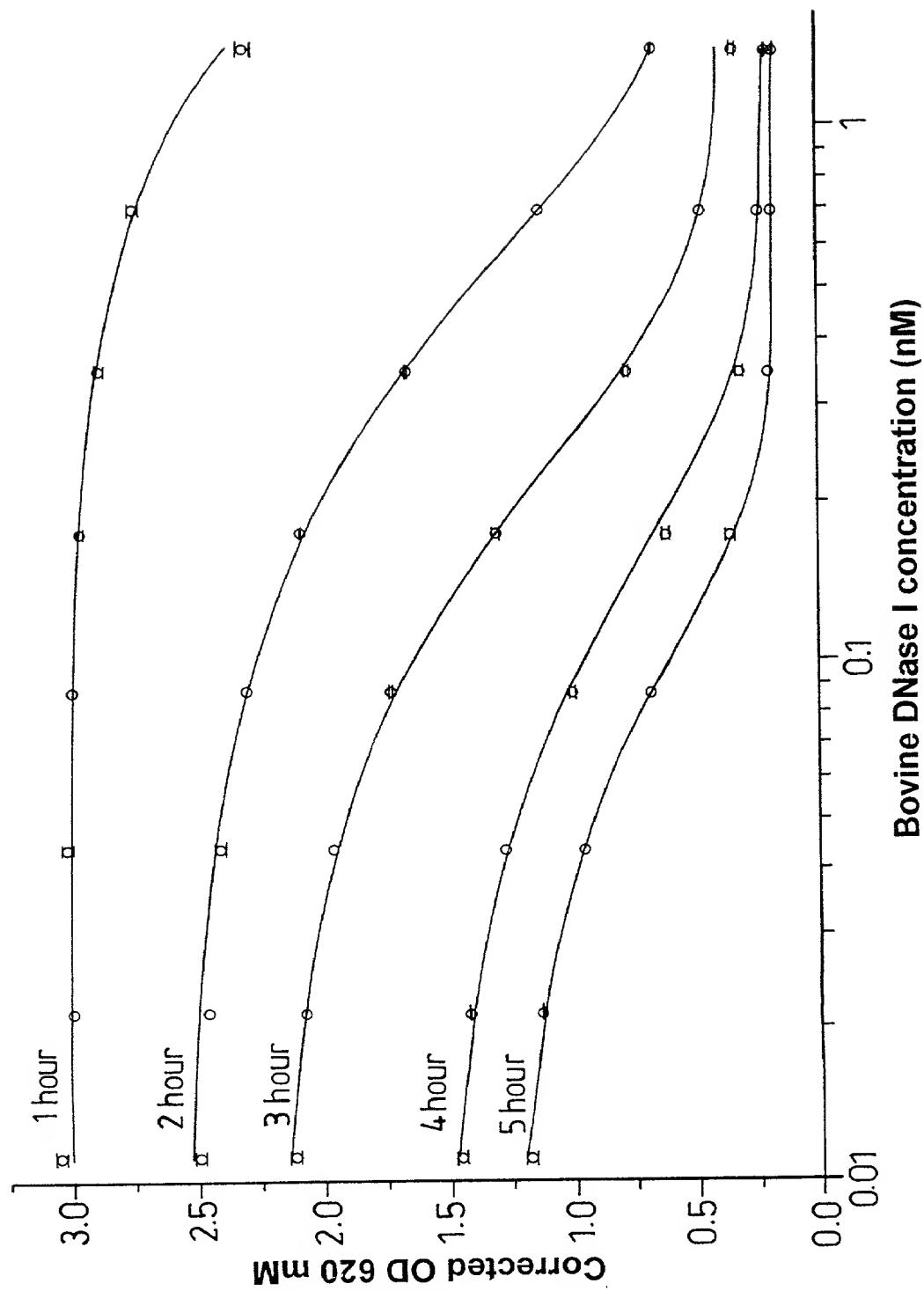


Fig. 23

Corrected bovine DNase I standard curves
at various time points



**Corrected DNase I activity in transiently expressed
humanised human HMFG1-human DNase I constructs**

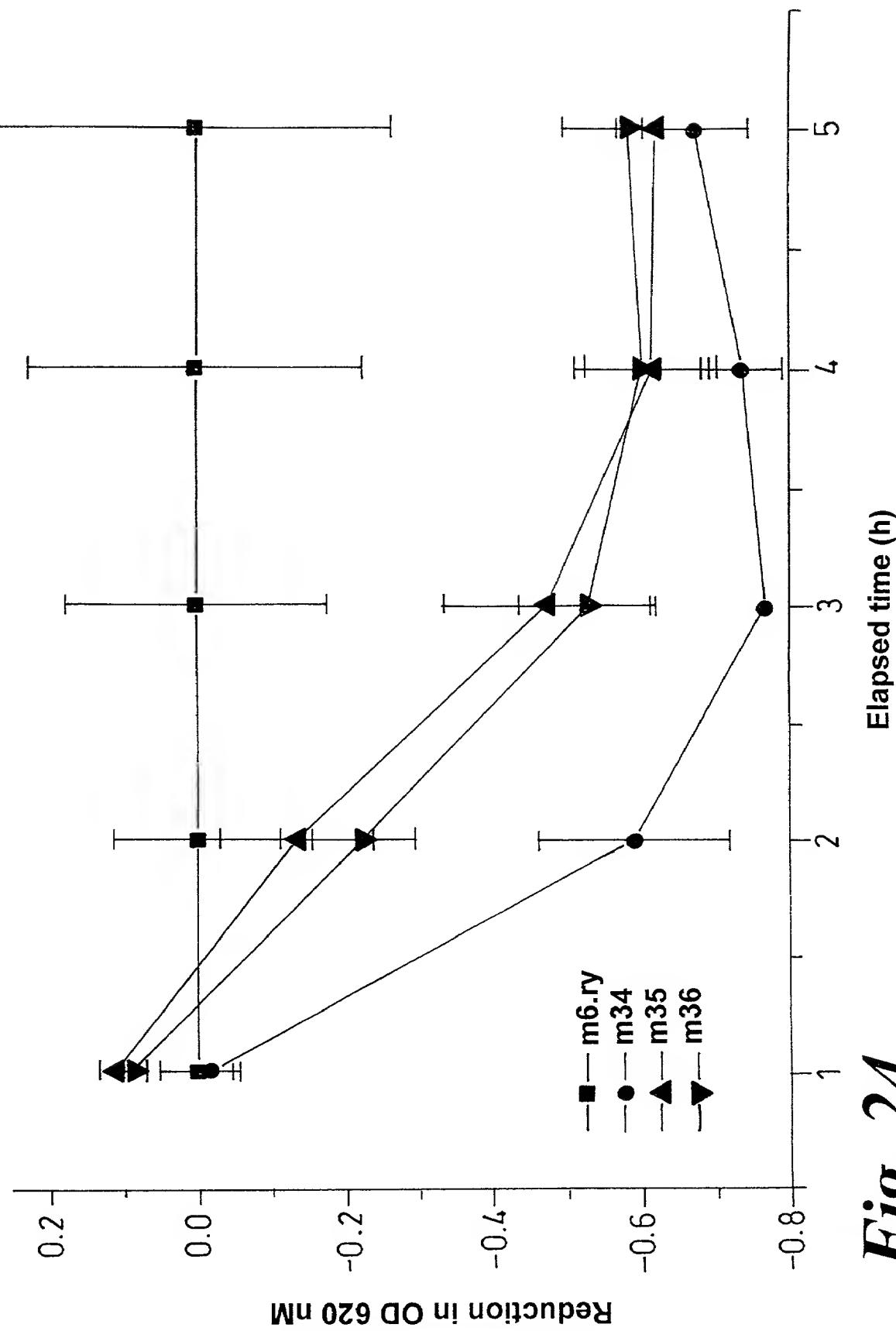


Fig. 24

Fig. 25

Corrected DNase I activity in transiently expressed
humanised HMFG1 F(ab')2-human DNase I fusions

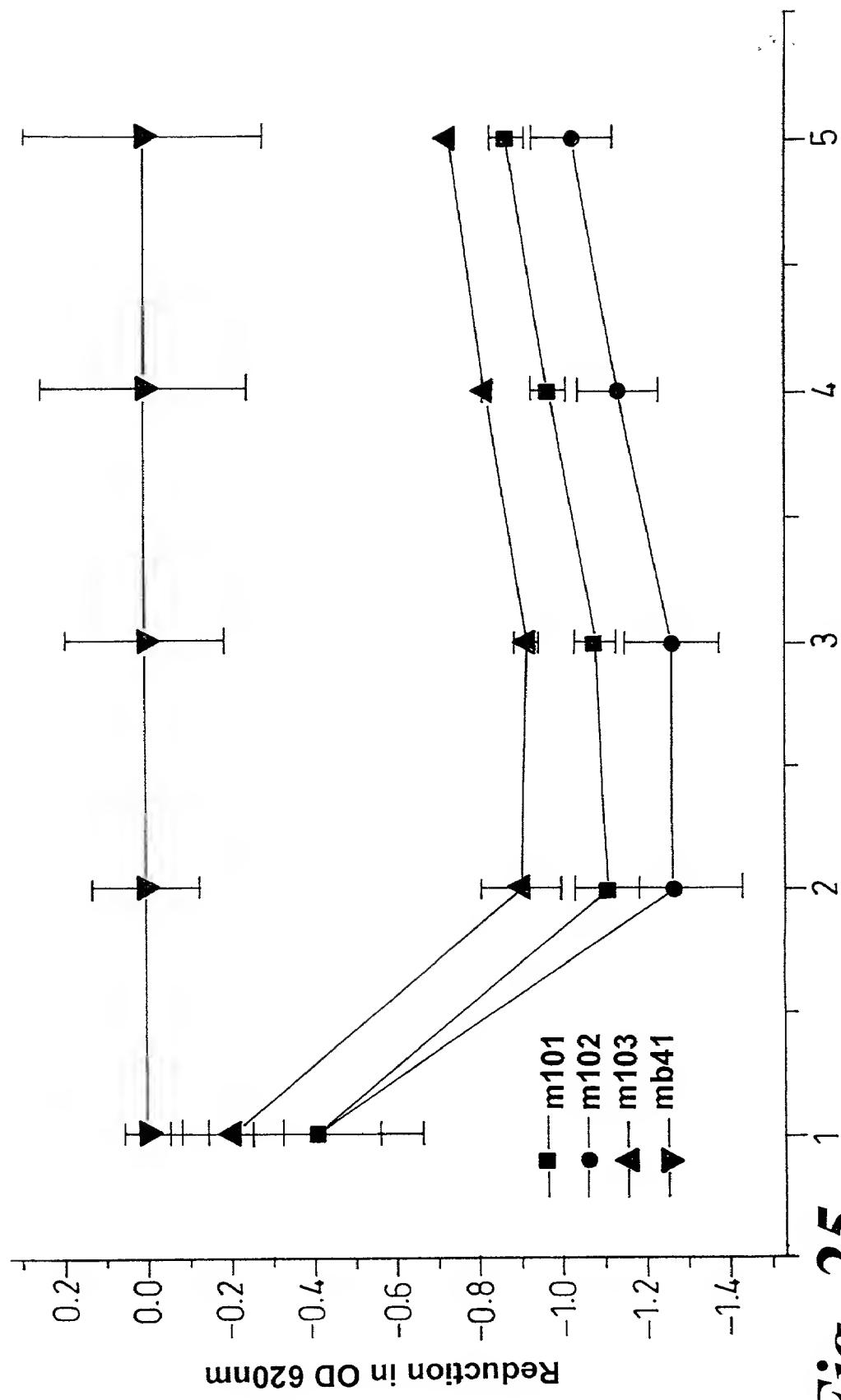


Fig. 26

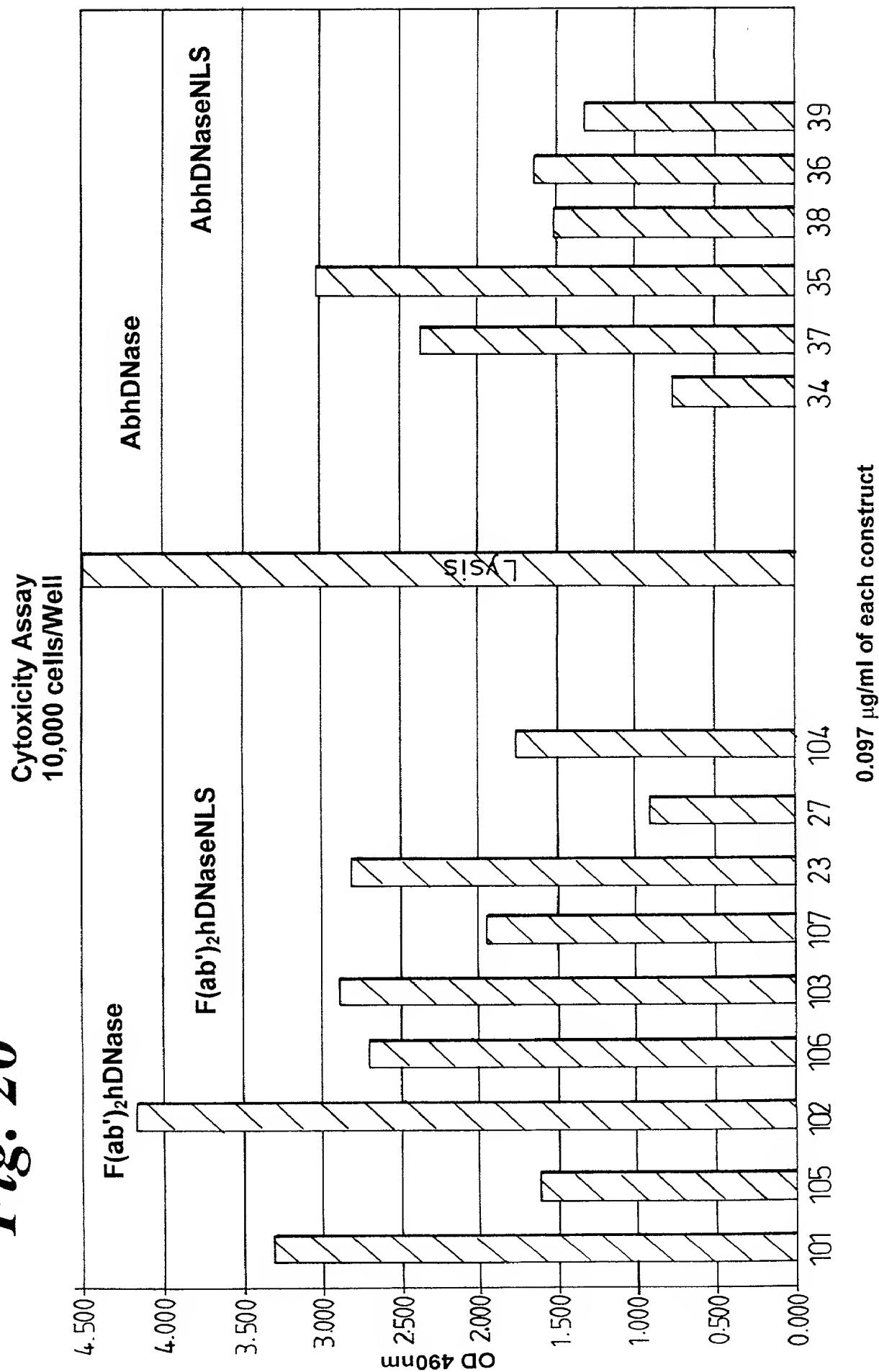
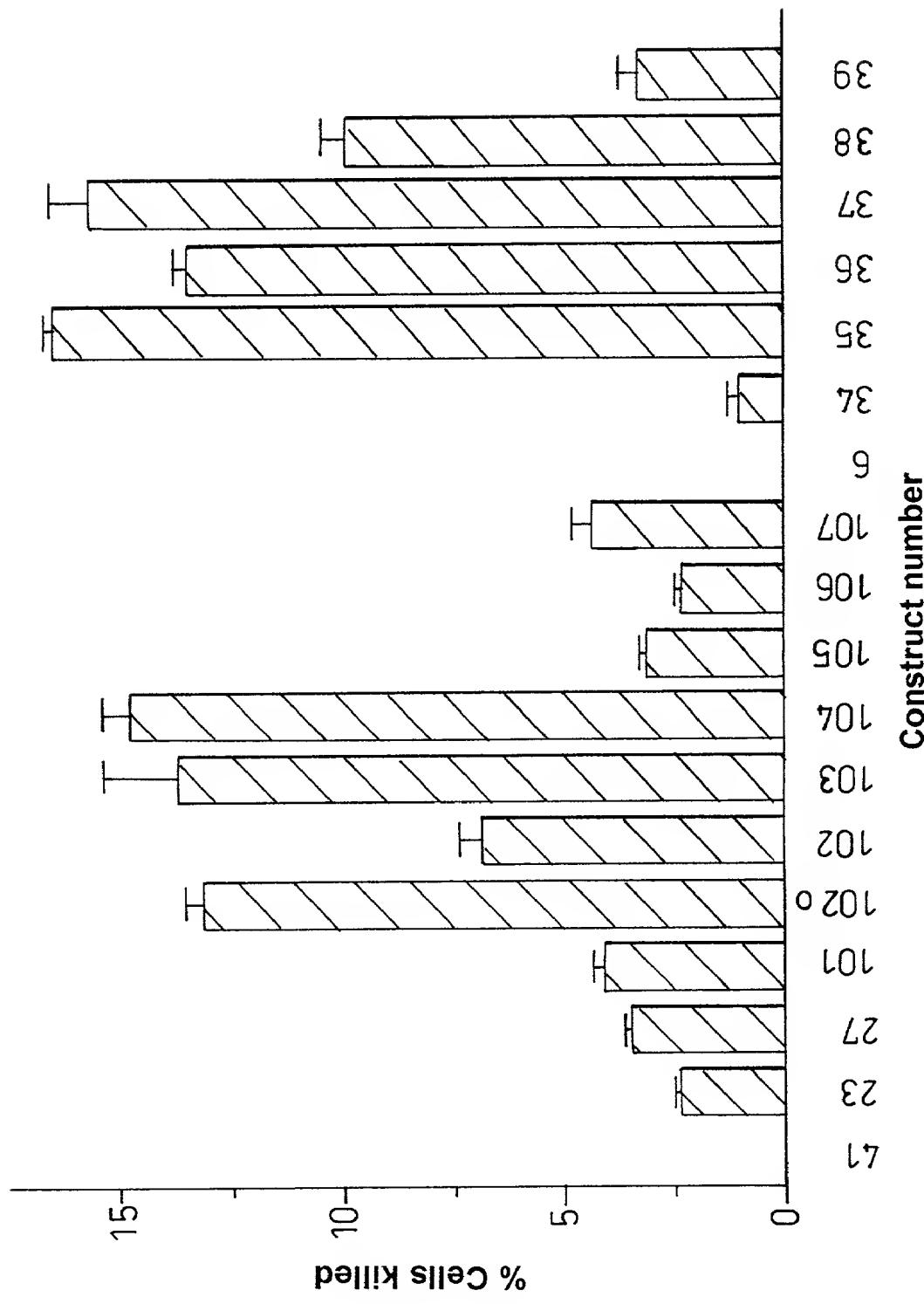


Fig. 27

MCF7 cells killed after 1h incubation with 1.35 ng of sample



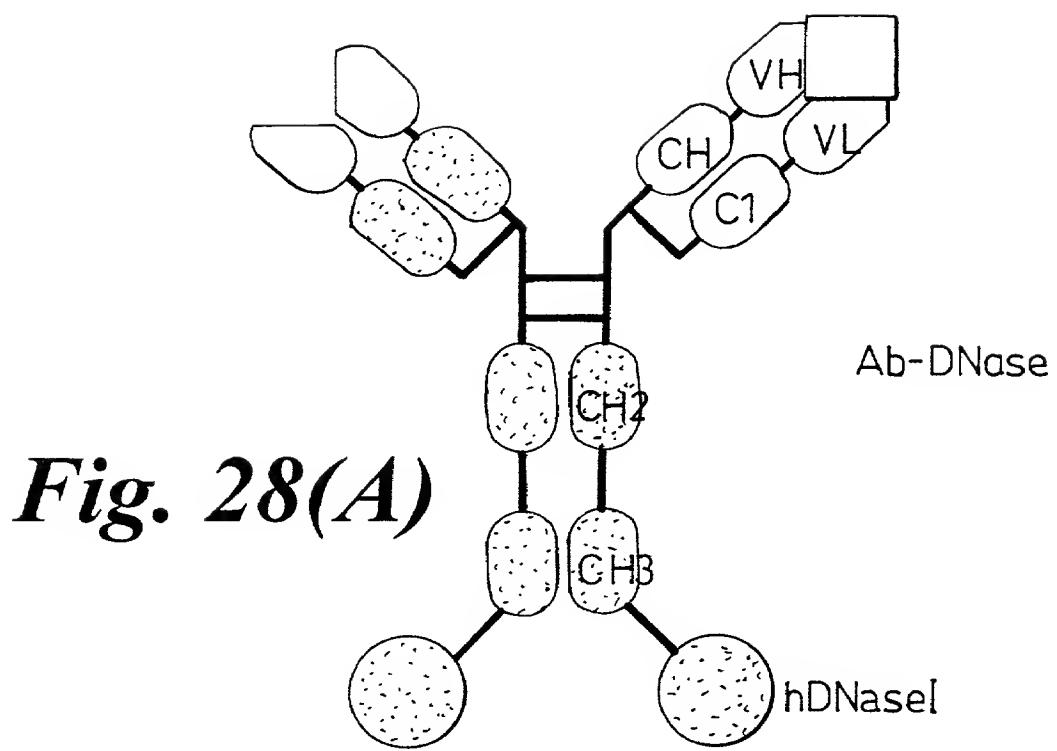


Fig. 28(A)

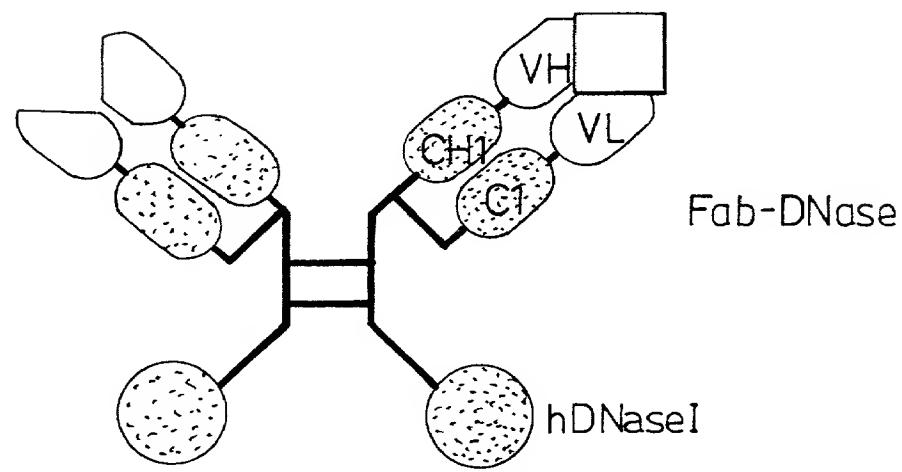
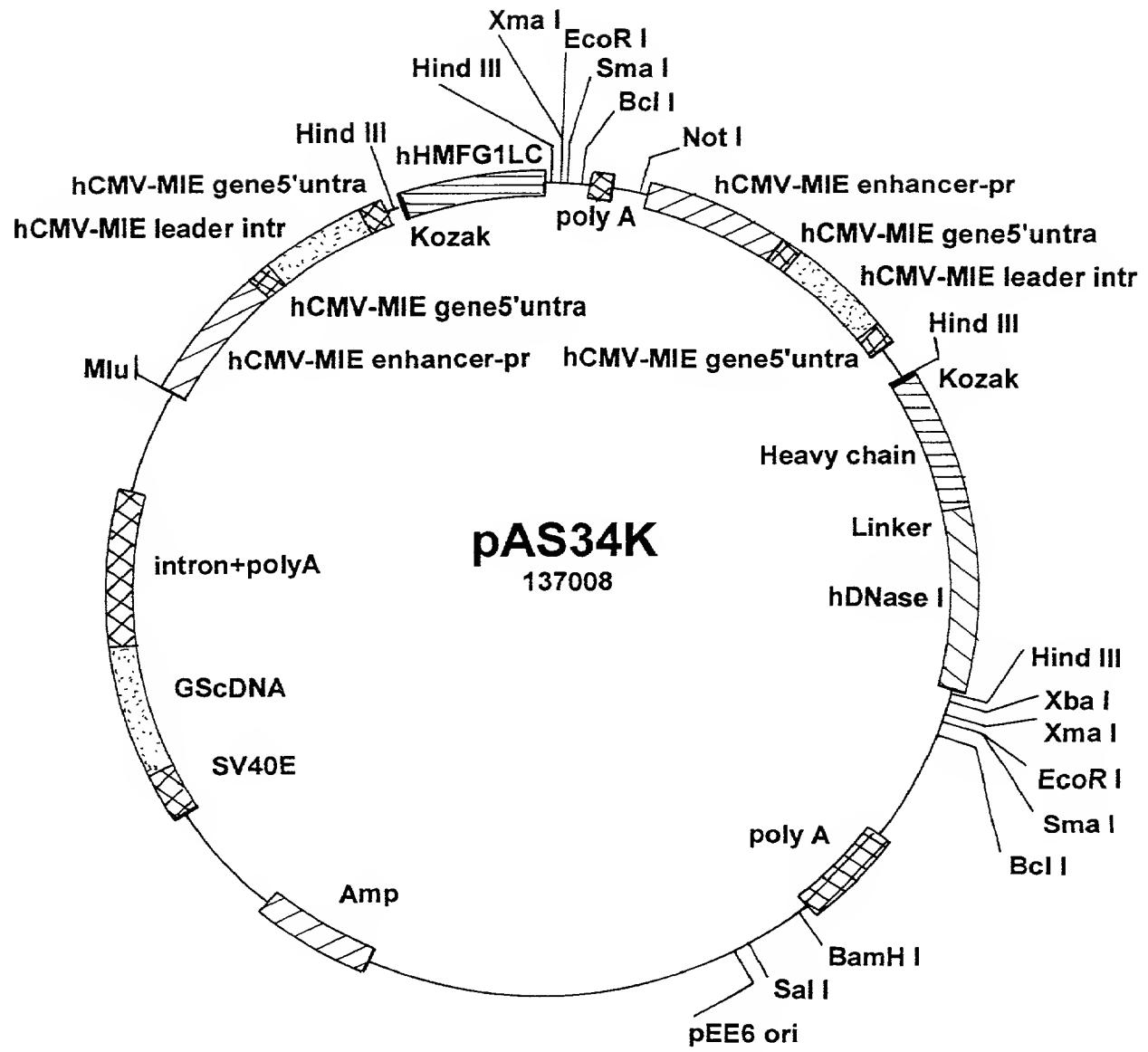
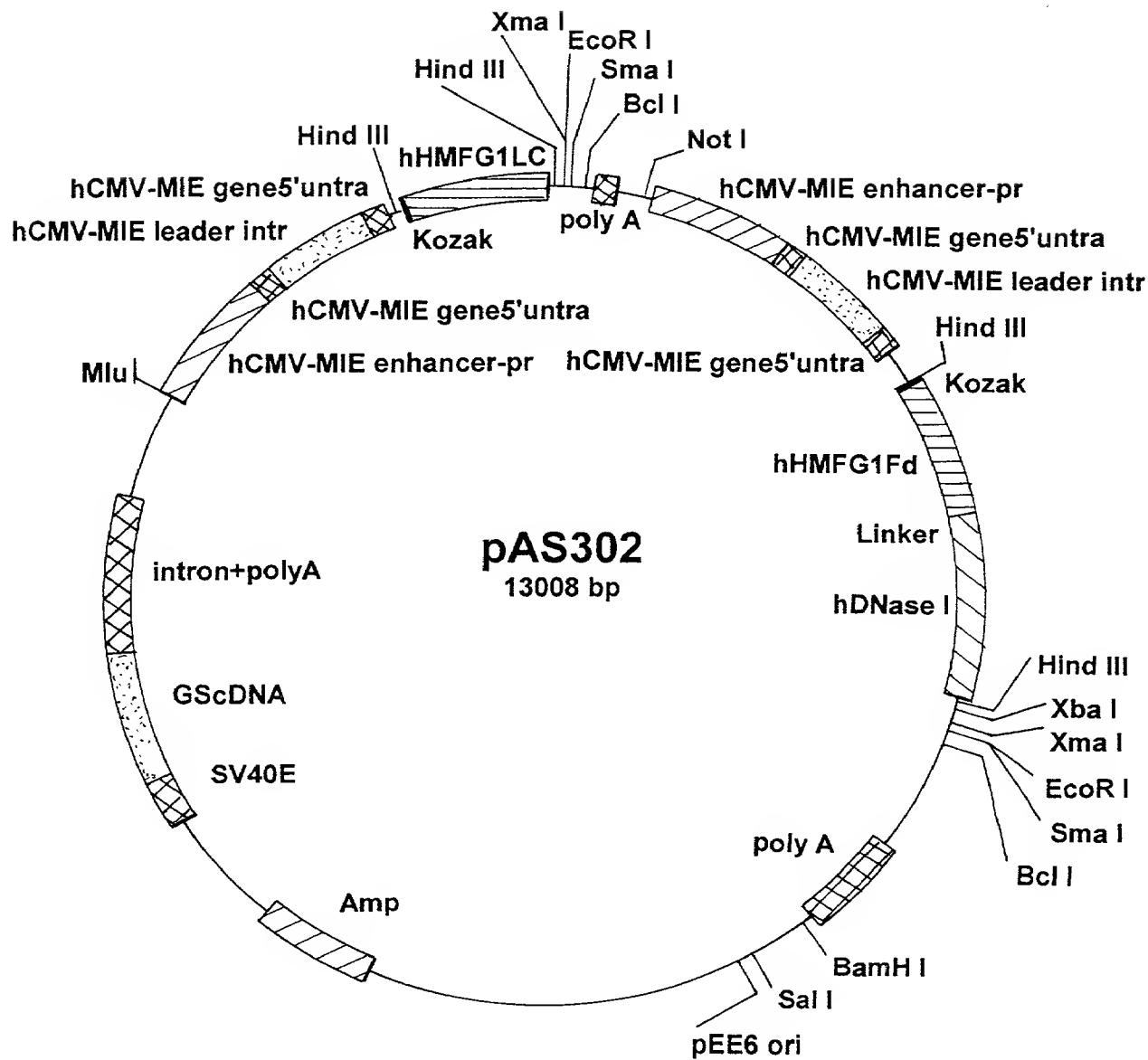


Fig. 28(B)



Ab-DNase

Fig. 29



Fab-DNase

Fig. 30

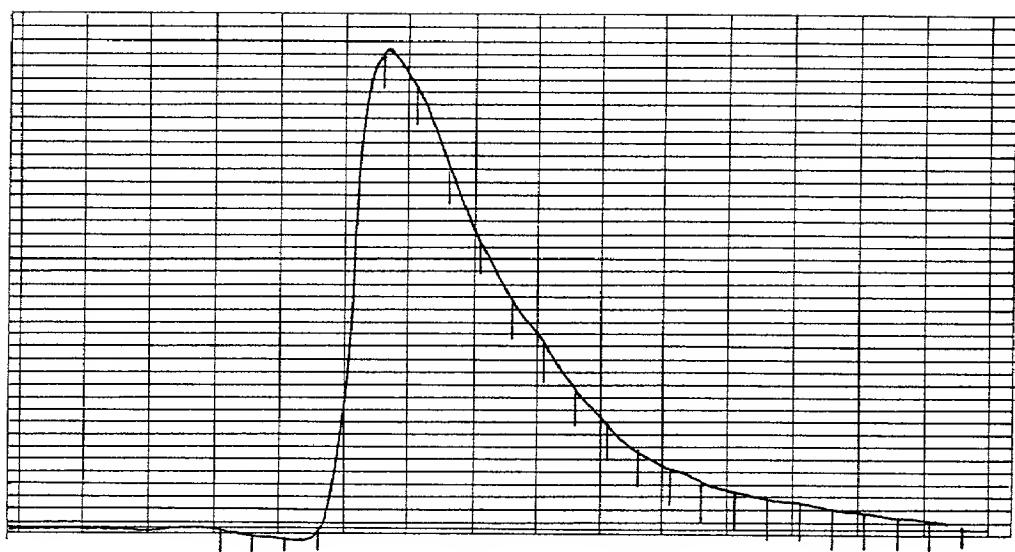


Fig. 31(A)

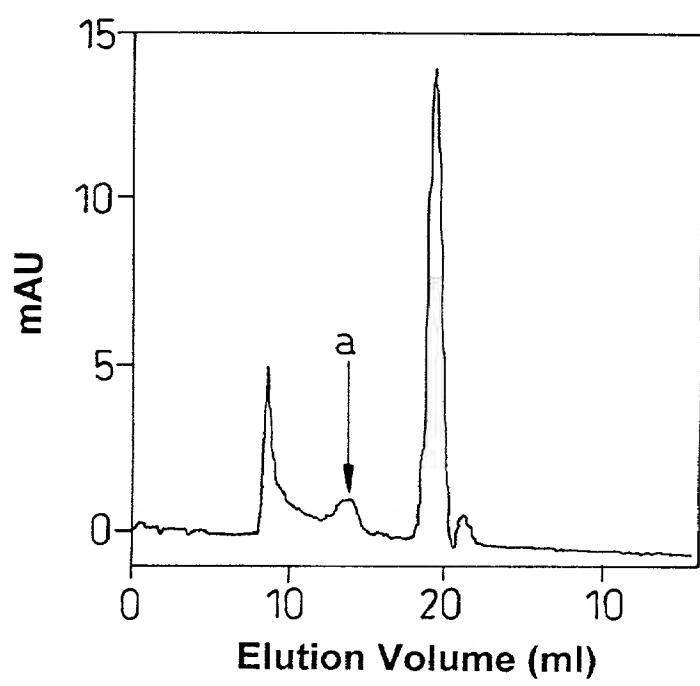


Fig. 31(B)

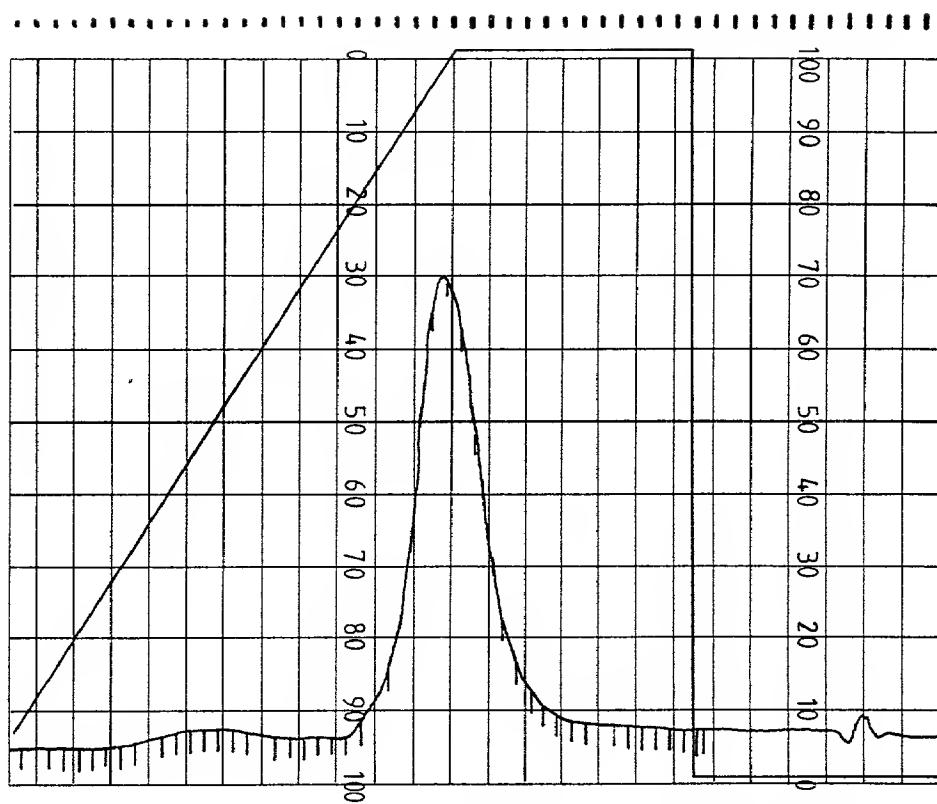


Fig. 32(A)

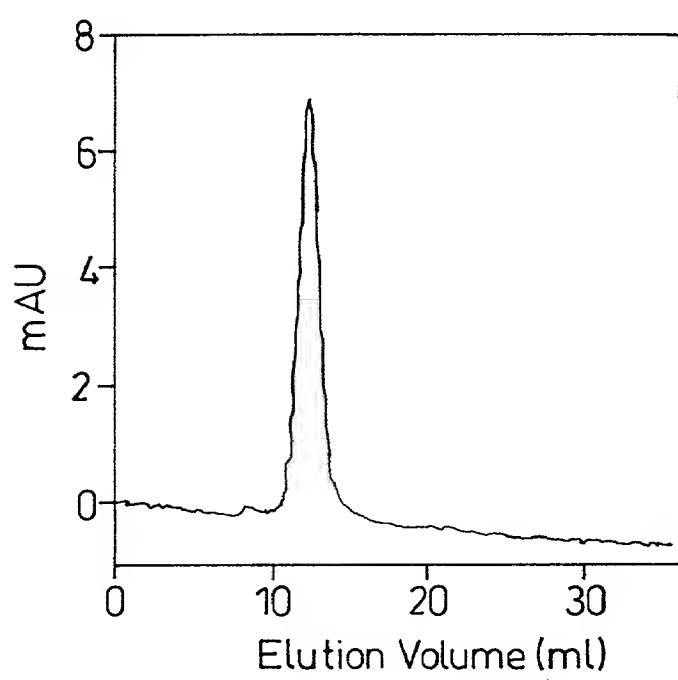


Fig. 32(B)

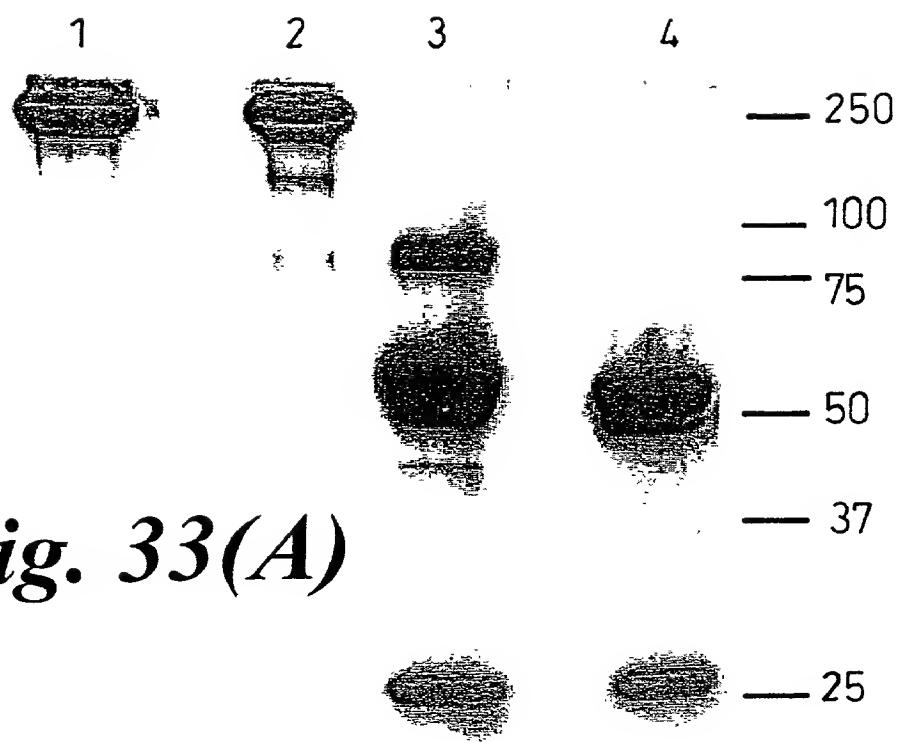


Fig. 33(A)

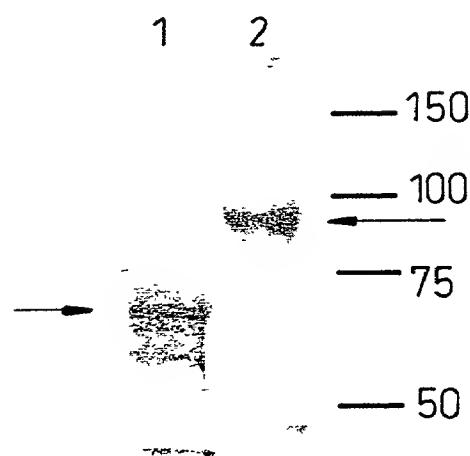


Fig. 33(B)

Bovine DNase I standard curves at various time points

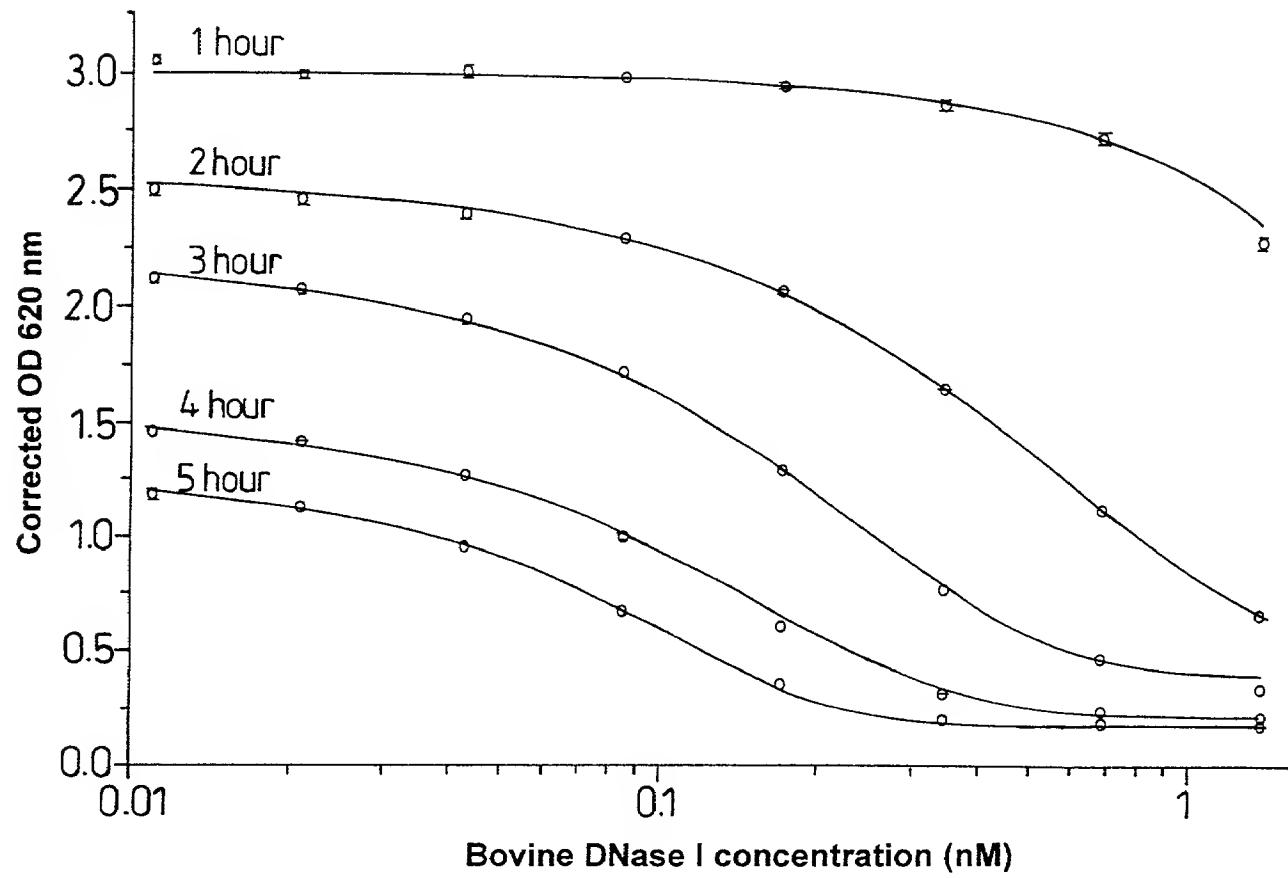


Fig. 34(A)

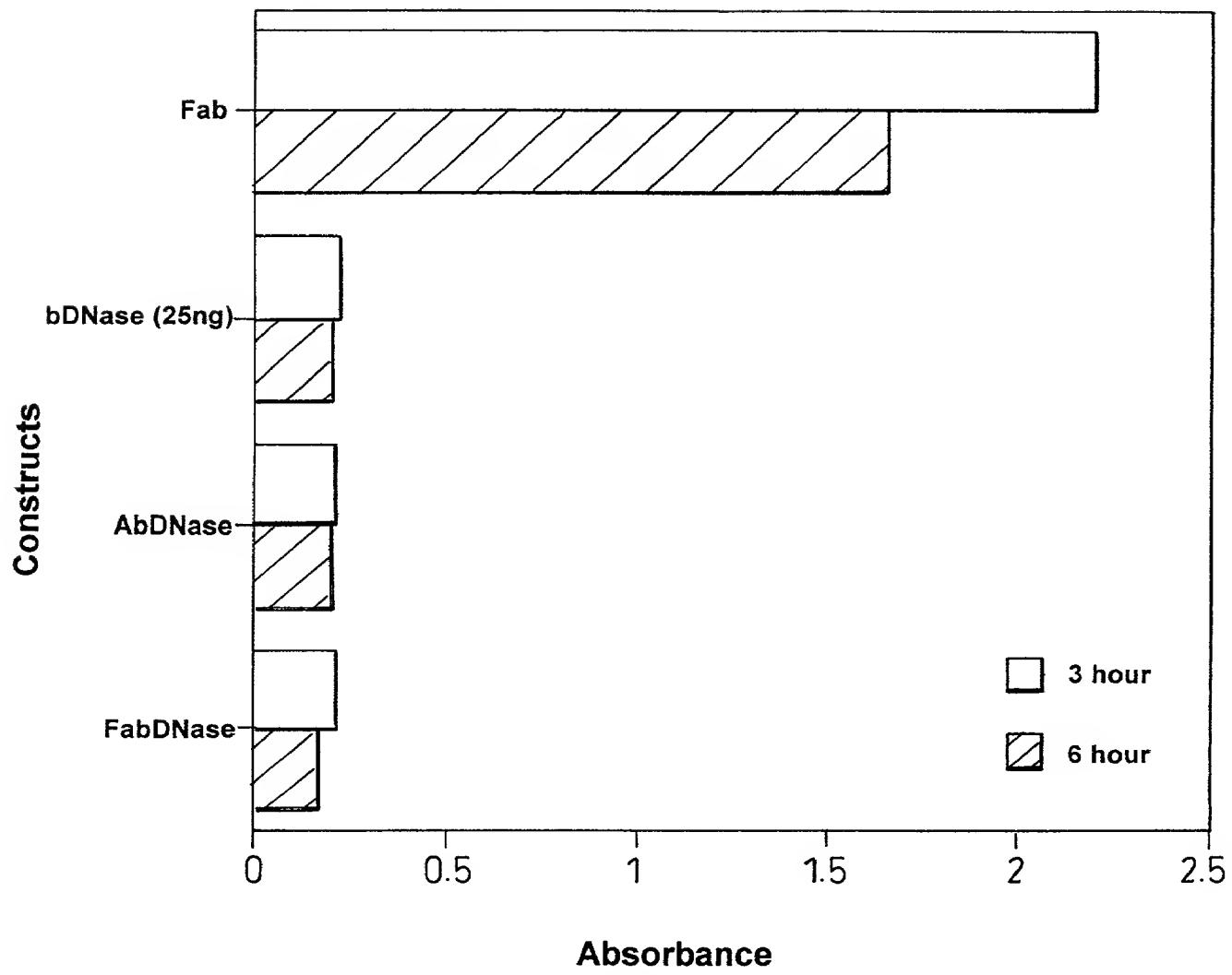


Fig. 34(B)

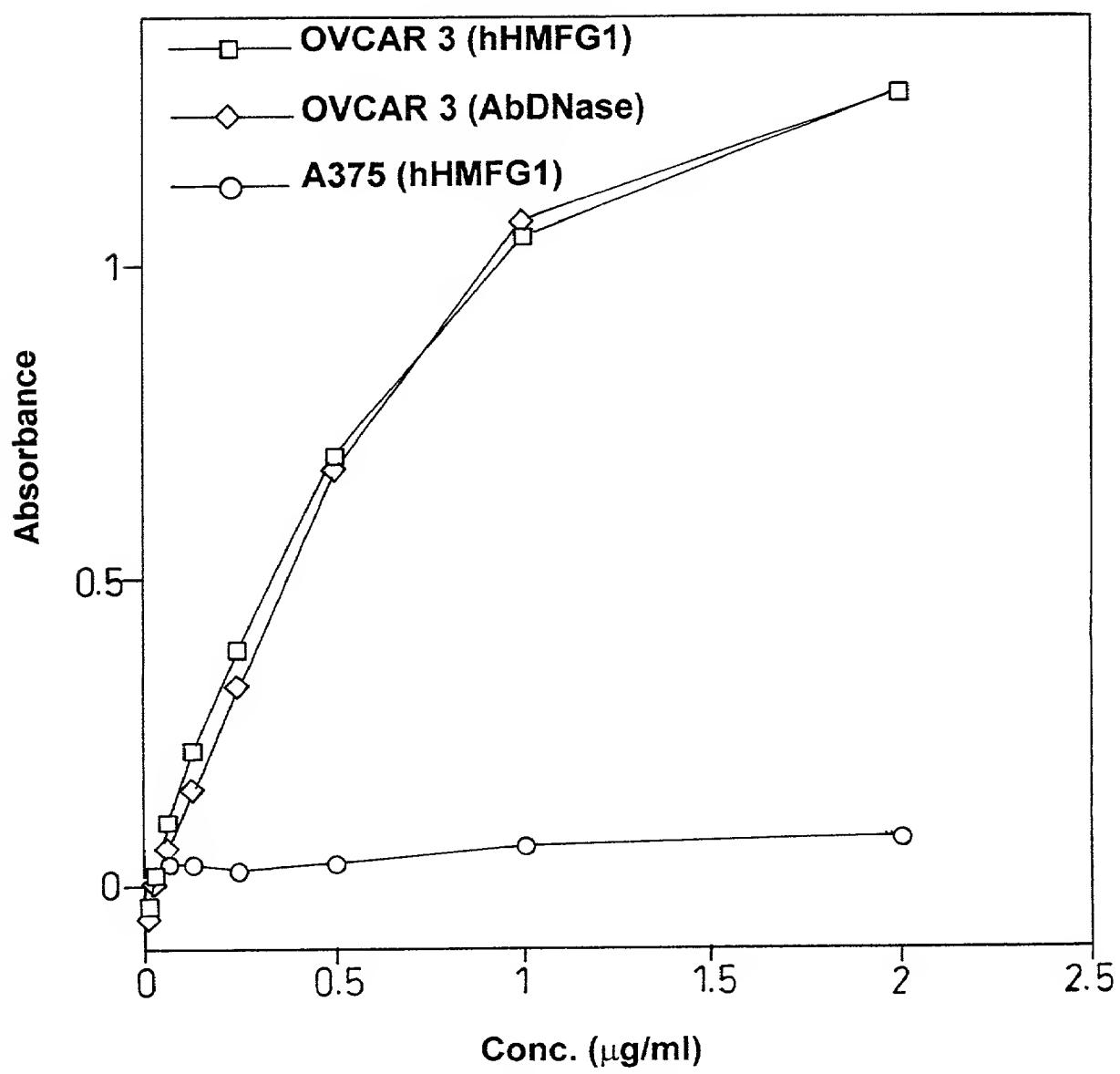


Fig. 35(A)

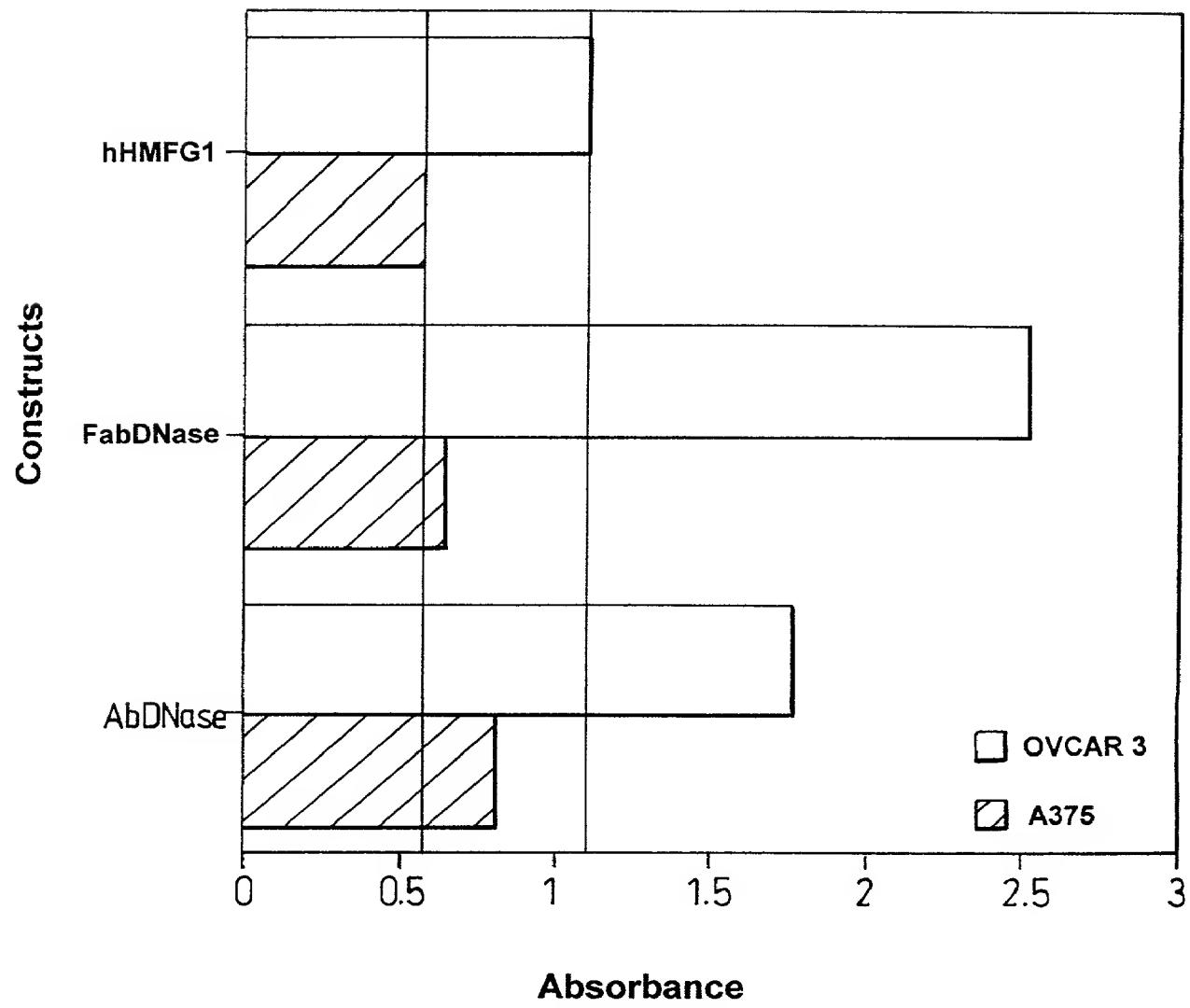


Fig. 35(B)